

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: October 24, 2004, 11:03:18 ; Search time 137 Seconds

(without alignments)
1885.717 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MLAVPASRNSQSSDVTDOGY.....SFVRLSFARSGDWAECEFA 449

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2353	99.8	467	1	PHYA ASPNG
2	2324	98.6	467	2	Q6T9Z6
3	2324	98.6	467	2	AAR08366
4	2313	98.1	467	2	Q9U0Z7
5	2309	97.9	467	1	PHYA ASPAW
6	2279	96.6	448	2	Q8U255
7	2278	96.6	448	2	Q6J336
8	2278	96.6	448	2	AAT12504
9	2278	96.6	467	2	Q93838
10	2273	96.4	448	2	Q6GYA8
11	2268	96.2	467	2	Q9HEQ0
12	2265	96.1	467	2	Q6R519
13	2265	96.1	467	2	AAS00648
14	1617.5	68.6	465	1	PHYA ASPFU
15	1610	68.3	466	2	Q9C1T1
16	1605.5	68.1	442	2	Q8WZJ5
17	1534	65.1	463	1	PHYB EMENI
18	1520	64.5	466	2	Q00100
19	1501.5	63.7	466	2	Q00096
20	1493	63.3	466	1	PHYA ASPTE
21	1475	62.6	461	2	Q6YNE9
22	1475	62.6	461	2	AAL55406
23	1177	49.9	596	2	Q7S9V5
24	1135	48.1	487	1	PHYA THIEH
25	765.5	32.5	443	2	Q96VF5
26	752.5	31.9	439	2	Q96VH9
27	739.5	31.4	453	2	Q96VT0
28	732	31.3	442	2	Q96VK9
29	732	31.0	442	2	Q96VK8
30	438	18.6	610	2	Q7SSH2
31	396	16.8	464	2	Q6BUR8

RESULT 1

ID	PHYA ASPNG	STANDARD;	PRT;	467 AA.
AC	P34752;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexakisphosphate 3-phosphohydrolase A) (3 phytase A) (Myo-inositol hexakisphosphate phosphohydrolase A).			
DE	Phosphohydrolase A.			
GN	Name=PHYA;			
OS	Aspergillus niger.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.			
OX	NCBI_TaxID=5061;			
RN	[1]			
RC	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	STRAIN=NRRL 3135 / Van Tieghem / Ficum;			
RX	MEDLINE=93252284; PubMed=8387447;			
RA	van Hartingsveldt W., van Zeijl C.M.J., Harteveld G.M., Gouka R.J.,			
RA	Suykerbyk M.E.G., Luiten R.G.M., van Paridon P.A., Saiten G.C.M.,			
RA	Veenstra A.E., van Gorcom R.F.W., van den Hondel C.A.M.J.J.;			
RT	"Cloning, characterization and overexpression of the phytase-encoding gene (phyA) of Aspergillus niger.";			
RL	Gene 127:87-94 (1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	Mullaney E.J.;			
RT	"Sequence of the Aspergillus niger (ficuum) phytase gene.";			
RL	Submitted (JUN-1992) to the EMBL/GenBank/DBSJ databases.			
RN	[3]			
RP	SEQUENCE OF 24-464.			
RC	STRAIN=NRRL 3135 / Van Tieghem / Ficum;			
RX	MEDLINE=93249451; PubMed=8387289;			
RA	Ullah A.H.J., Dischinger H.C. Jr.;			
RT	"Aspergillus ficuum phytase: complete primary structure elucidation by chemical sequencing.";			
RL	Biochem. Biophys. Res. Commun. 192:747-753 (1993).			
RN	[4]			
RP	SEQUENCE OF 71-93.			
RC	STRAIN=NRRL 3135 / Van Tieghem / Ficum;			
RX	MEDLINE=91298982; PubMed=1648914;			
RA	Ullah A.H.J., Cummins B.J., Dischinger H.C. Jr.;			
RT	"Cyclohexanediol modification of arginine at the active site of Aspergillus ficuum phytase.";			
RL	Biochem. Biophys. Res. Commun. 178:45-53 (1991).			
RN	[5]			
RP	CHARACTERIZATION, AND PARTIAL SEQUENCE.			
RC	STRAIN=NRRL 3135 / Van Tieghem / Ficum;			
RX	MEDLINE=89160685; PubMed=2852807;			
RA	Ullah A.H.J.;			
RT	"Aspergillus ficuum phytase: partial primary structure, substrate selectivity, and kinetic characterization.";			
RL	Prep. Biochem. 18:459-471 (1988).			

32	394.5	16.7	461	2	Q6BM79	Q6bm79 debaryomyce
33	393	16.7	584	2	Q6CCS5	Q6ccs5 yarrowia li
34	386	16.4	469	2	Q6CSM6	Q6csm6 kluyveromyc
35	385	16.3	467	1	PPA3_YEAST	P24031 saccharomyc
36	385	16.3	467	1	PPA5_YEAST	P06335 saccharomyc
37	382	16.2	469	2	Q6CYI2	Q6cyi2 kluyveromyc
38	368	15.6	468	1	PPAD_YEAST	P22290 saccharomyc
39	357	15.1	469	2	Q9Y846	Q9y846 kluyveromyc
40	357	15.1	482	2	Q8X1W7	Q8x1w7 monascus an
41	354	15.0	469	2	Q6CWZ7	Q6cwz7 kluyveromyc
42	353	15.0	469	1	PPAS_KLULA	P52289 kluyveromyc
43	352	14.9	467	1	PPAB_YEAST	P38442 saccharomyc
44	352	14.9	467	1	PPAC_YEAST	P38693 saccharomyc
45	343	14.5	484	2	Q6CLW3	Q6clw3 kluyveromyc

ALIGNMENTS


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QY 302 ANELIARLTHSPVHDDTSSNHTLSDSPATFPPLNSTLYADFSDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLSDSPATFPPLNSTLYADFSDNGIISILFALGLYNGTK 379
QY 362 PLSTTTTVENITQTDGFSASAWTPPFASRLYVENMQCAEQEPLRVLVNDRVVPVPLHGCPVD 421
DB 380 PLSTTTTVENITQTDGFSASAWTPPFASRLYVENMQCAEQEPLRVLVNDRVVPVPLHGCPVD 439
QY 422 ALGRCRTRDSFVRGLSFARSGGDWAECEFA 449
DB 440 ALGRCRTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 2
Q6T9Z6 PRELIMINARY; PRT; 467 AA.
ID Q6T9Z6;
AC Q6T9Z6;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Phytase.
GN Name=phyA;
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]_TaxID=5061;
RP SEQUENCE FROM N.A.
RC STRAIN=N14*;
RA Peng Y.Y., Zhou Z.Y., Ma L.P.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR InterPro; IPR000560; HisAc_phosphatase.
DR Pfam; PF0328; Acid_phosphatase; 1.
DR PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.
DR PROSITE; PS00778; HIS ACID PHOSPHAT 2; 1.
SQ SEQUENCE 467 AA; 51142 MW; 2EAECD38865E94EF CRC64;

Query Match 98.6%; Score 2324; DB 2; Length 467;
Best Local Similarity 98.0%; Pred. No. 6.2e-165;
Matches 439; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 LAVPASRNQSCDVTVDQGYQCFSETSHLWQYAPFPFSLANESVISPEVPAGCRVTFAQVL 61
DB 20 LAVPASRNQSCDVTVDQGYQCFSETSHLWQYAPFPFSLANESVISPEVPAGCRVTFAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEHQQNATTFDGKYAFLKTYNYSGLGADDLTPFGEOELVNS 121
DB 80 SRHGARYPTDSKGGKYSALIEHQQNATTFDGKYAFLKTYNYSGLGADDLTPFGEOELVNS 139
QY 122 GIKFYQRYESLNTNIVPFRSSGSRVTSAGKKFIEGFQSTKLDKDPRAQPGOSSPKIDVV 181
DB 140 GIKFYQRYESLNTNIVPFRSSGSRVTSAGKKFIEGFQSTKLDKDPRAQPGOSSPKIDVV 199
QY 182 ISEASSNNLDPGCTVTFEDSELADTVANFTATFVPSIRQRLNDLSGVLTDTTEVTY 241
DB 200 ISEASSNNLDPGCTVTFEDSELADTVANFTATFVPSIRQRLNDLSGVLTDTTEVTY 259
QY 242 LDMCSEFDTISTNTVDTKLSPFCDLFTHEWINYDYLQSLKKYGHGAGNPLGPTQGVGY 301
DB 260 LDMCSEFDTISTNTVDTKLSPFCDLFTHEWINYDYLQSLKKYGHGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLSDSPATFPPLNSTLYADFSDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLSDSPATFPPLNSTLYADFSDNGIISILFALGLYNGTK 379
QY 362 PLSTTTTVENITQTDGFSASAWTPPFASRLYVENMQCAEQEPLRVLVNDRVVPVPLHGCPVD 421
DB 380 PLSTTTTVENITQTDGFSASAWTPPFASRLYVENMQCAEQEPLRVLVNDRVVPVPLHGCPVD 439
QY 422 ALGRCRTRDSFVRGLSFARSGGDWAECEFA 449
DB 440 ALGRCRTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 4
Q9UUZ7 PRELIMINARY; PRT; 467 AA.
ID Q9UUZ7;
AC Q9UUZ7;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMELrel. 26, Last annotation update)
DE Myo-inositol hexaphosphate phosphohydrolyase precursor (EC 3.1.3.8).
DE Aspergillus niger.

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DB 440 ALGRCRTRDSFVKGLSFARSGGDWAECEFA 467

RESULT 3
AAR08366 PRELIMINARY; PRT; 467 AA.
ID AAR08366;
AC AAR08366;
DT 02-MAR-2004 (TREMELrel. 27, Created)
DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)
DE Phytase.
GN PHA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]_TaxID=5061;
RP SEQUENCE FROM N.A.
RC STRAIN=N14*;
RA Peng Y.Y., Zhou Z.Y., Ma L.P.;
RL "Cloning and characterization of phytase gene of Aspergillus niger N14*.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY426977; AAR08366.1; -. 2EAECD38865E94EF CRC64;
SQ SEQUENCE 467 AA; 51142 MW; 2EAECD38865E94EF CRC64;

Query Match 98.6%; Score 2324; DB 2; Length 467;
Best Local Similarity 98.0%; Pred. No. 6.2e-165;
Matches 439; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 LAVPASRNQSCDVTVDQGYQCFSETSHLWQYAPFPFSLANESVISPEVPAGCRVTFAQVL 61
DB 20 LAVPASRNQSCDVTVDQGYQCFSETSHLWQYAPFPFSLANESVISPEVPAGCRVTFAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEHQQNATTFDGKYAFLKTYNYSGLGADDLTPFGEOELVNS 121
DB 80 SRHGARYPTDSKGGKYSALIEHQQNATTFDGKYAFLKTYNYSGLGADDLTPFGEOELVNS 139
QY 122 GIKFYQRYESLNTNIVPFRSSGSRVTSAGKKFIEGFQSTKLDKDPRAQPGOSSPKIDVV 181
DB 140 GIKFYQRYESLNTNIVPFRSSGSRVTSAGKKFIEGFQSTKLDKDPRAQPGOSSPKIDVV 199
QY 182 ISEASSNNLDPGCTVTFEDSELADTVANFTATFVPSIRQRLNDLSGVLTDTTEVTY 241
DB 200 ISEASSNNLDPGCTVTFEDSELADTVANFTATFVPSIRQRLNDLSGVLTDTTEVTY 259
QY 242 LDMCSEFDTISTNTVDTKLSPFCDLFTHEWINYDYLQSLKKYGHGAGNPLGPTQGVGY 301
DB 260 LDMCSEFDTISTNTVDTKLSPFCDLFTHEWINYDYLQSLKKYGHGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLSDSPATFPPLNSTLYADFSDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLSDSPATFPPLNSTLYADFSDNGIISILFALGLYNGTK 379
QY 362 PLSTTTTVENITQTDGFSASAWTPPFASRLYVENMQCAEQEPLRVLVNDRVVPVPLHGCPVD 421
DB 380 PLSTTTTVENITQTDGFSASAWTPPFASRLYVENMQCAEQEPLRVLVNDRVVPVPLHGCPVD 439
QY 422 ALGRCRTRDSFVRGLSFARSGGDWAECEFA 449
DB 440 ALGRCRTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 4
Q9UUZ7 PRELIMINARY; PRT; 467 AA.
ID Q9UUZ7;
AC Q9UUZ7;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMELrel. 26, Last annotation update)
DE Myo-inositol hexaphosphate phosphohydrolyase precursor (EC 3.1.3.8).
DE Aspergillus niger.

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OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hongning W., Qi W., Jing X.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF218813; AAF25481.1; -;
 DR HSP; P34752; 11HP.
 DR GO; GO:0003933; F:acid phosphatase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR InterPro; IPR000560; HisAc phspase.
 DR Pfam; PF00328; Acid phosphat A; 1.
 DR PROSITE; PS00616; HIS ACID PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS ACID PHOSPHAT_2; 1.
 KW Hydrolase; Lyase; Signal.
 FT SIGNAL 1 19 Potential.
 SQ SEQUENCE 467 AA; 51029 MW; F4300A8F165BEF92 CRC64;
 Query Match 98.1%; Score 2313; DB 2; Length 467;
 Best Local Similarity 97.5%; Pred. No. 4.1e-164;
 Matches 43; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
 QY 2 LAVPASRNSQSCDVTVDQGYQCFSTSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 61
 DB 20 LAVPASRNSQSCDVTVDQGYQCFSTSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 79
 QY 62 SRHGARYPTDSKGGKYSALIEIQONATTPDGKVAFLKTYNSLGADDLTPFGQELVNS 121
 DB 80 SRHGARYPTDSKGGKYSALIEIQONATTPDGKVAFLKTYNSLGADDLTPFGQELVNS 139
 QY 122 GIKFYQRYESLTRNIVPFISSGSSRVIASGKPIEGFQSTKLDPRAQPGQSSPKIDVV 181
 DB 140 GIKFYQRYESLTRNIVPFISSGSSRVIASGKPIEGFQSTKLDPRAQPGQSSPKIDVV 199
 QY 122 GIKFYQRYESLTRNIVPFISSGSSRVIASGKPIEGFQSTKLDPRAQPGQSSPKIDVV 181
 DB 140 GIKFYQRYESLTRNIVPFISSGSSRVIASGKPIEGFQSTKLDPRAQPGQSSPKIDVV 199
 QY 182 ISASSSNNLTDPGTCVTFDESELADTVEANFTATFVPSIRORLENDLSGVTLTDTVTY 241
 DB 200 ISASSSNNLTDPGTCVTFDESELADTVEANFTATFVPSIRORLENDLSGVTLTDTVTY 259
 RESULT 5
 PHVA ASPAW
 ID PHVA ASPAW STANDARD; PRT; 467 AA.
 AC P34753;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate 3-phosphohydrolase A)
 DE Name=PHYA; Synonyms=PHY;
 OS Aspergillus awamori.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=105351;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=ALK0243;
 RX MEDLINE=9400796; PubMed=8224894;
 RA Piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A.,
 RA Miettinen-Oinonen A., Nevalainen H., Rambosc J.A.;
 RT "The cloning and sequencing of the genes encoding phytase (phy) and pH
 RT 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
 RT awamori";
 RL Gene 133:55-62(1993).
 CC -!- FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate
 CC from phytate.
 CC -!- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = 1D-
 CC myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate.
 CC -!- SUBCELLULAR LOCATION: Secreted
 CC -!- SIMILARITY: Belongs to the histidine acid phosphatase family.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC EMBL; L02421; AAA16898.1; -;
 DR PIR; JN0889; JN0889.
 DR HSP; P34752; 11HP.
 DR InterPro; IPR000560; HisAc_phspase.
 DR Pfam; PF00328; Acid phosphat A; 1.
 DR PROSITE; PS00616; HIS ACID PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS ACID PHOSPHAT_2; 1.
 KW Glycoprotein; Hydrolase; Signal.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 467 3-Phytase A.
 FT ACT_SITE 82 82 Nucleophile (By similarity).
 FT ACT_SITE 362 362 Proton donor (By similarity).
 FT DISULFID 31 40 By similarity.
 FT DISULFID 71 414 By similarity.
 FT DISULFID 215 465 By similarity.
 FT DISULFID 264 282 By similarity.
 FT DISULFID 436 444 By similarity.
 FT CARBOHYD 27 27 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 59 59 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 105 105 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 120 120 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 207 207 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 230 230 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 339 339 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 352 352 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 376 376 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 388 388 N-linked (GLCNAC. .) (Potential).
 SQ SEQUENCE 467 AA; 51074 MW; 1189828A5D7EC661 CRC64;
 Query Match 97.9%; Score 2309; DB 1; Length 467;
 Best Local Similarity 97.3%; Pred. No. 8.2e-164;
 Matches 436; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 2 LAVPASRNSQSCDVTVDQGYQCFSTSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 61
 DB 20 LAVPASRNSQSCDVTVDQGYQCFSTSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 79
 QY 62 SRHGARYPTDSKGGKYSALIEIQONATTPDGKVAFLKTYNSLGADDLTPFGQELVNS 121
 DB 80 SRHGARYPTDSKGGKYSALIEIQONATTPDGKVAFLKTYNSLGADDLTPFGQELVNS 139
 QY 122 GIKFYQRYESLTRNIVPFISSGSSRVIASGKPIEGFQSTKLDPRAQPGQSSPKIDVV 181
 DB 140 GIKFYQRYESLTRNIVPFISSGSSRVIASGKPIEGFQSTKLDPRAQPGQSSPKIDVV 199
 QY 182 ISASSSNNLTDPGTCVTFDESELADTVEANFTATFVPSIRORLENDLSGVTLTDTVTY 241
 DB 200 ISASSSNNLTDPGTCVTFDESELADTVEANFTATFVPSIRORLENDLSGVTLTDTVTY 259

DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DE Phytase (Fragment).
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nong Y., He Y., Rachid L., Wu Z., Qing Y.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 FT EMBL; AY603416; AAT12504.1; -
 FT NON TER 1
 SQ SEQUENCE 448 AA; 49169 MW; FBABFCDE20140514 CRC64;

 Query Match 96.6%; Score 2278; DB 2; Length 448;
 Best Local Similarity 95.3%; Pred. No. 1.6e-161;
 Matches 427; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

 Qy 2 LAVPASRNQSSCDTVDQGYQCFSTSHLWGQYAPFFSLANESVTSPEVPAGCRVTFPAQVL 61
 Db 1 LAVPASRNQSSCDTVDQGYQCFSTSHLWGQYAPFFSLANESVTSPEVPAGCHVTFPAQVL 60

 Qy 62 SRHGARYPTDSKGKYSALIBEIQQNATTFPGKYAFKTKYNSLGADDLTPFGQELVNS 121
 Db 61 SRHGARYPTDSKGKYSALIBEIQQNATTFPGKYAFKTKYNSLGADDLTPFGQELVNS 120

 Qy 122 GIKFYQRYESLTRNIVPFIRSSGSRVIAAGKKEIEGFQSTKLDRAQPGQSSPKIDVV 181
 Db 121 GIKFYQRYESLTRNIVPFIRSSGSRVIAAGKKEIEGFQSTKLDRAQPGQSSPKIDVV 180

 Qy 182 ISEASSNNITDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVLTDTEVY 241
 Db 181 ISEASTNNITDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVLTDTEVY 240

 Qy 242 LMDMCSFDTTSTVDTKLSFPCDLFTHDEWINVDYLQSLKYYGHGAGNPLGPTQGVY 301
 Db 241 LMDMCSFDTTSTVDTKLSFPCDLFTHDEWINVDYLQSLKYYGHGAGNPLGPTQGVY 300

 Qy 302 ANELIARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSDHNGIISILFALGLYNGTK 361
 Db 301 ANELIARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSDHNGIISILFALGLYNGTK 360

 Qy 362 PLSTTTVENTITQDTGFSSAWTVFPASRLYVEMMQCQAEPLVRVLVNDRVVPLHGCPVD 421
 Db 361 PLSTTTAENITQDTGFSSAWTVFPASRLYVEMMQCQAEPLVRVLVNDRVVPLHGCPVD 420

 Qy 422 ALGRCRDSFVRGLSFARSGGDWAECEFA 449
 Db 421 ALGRCRDSFVRGLSFARSGGDWAECEFA 448

 RESULT 9
 O93838 PRELIMINARY; PRT; 467 AA.
 AC O93838
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DE Phytase.
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Aspergillus.
 OX NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nagashima T., Kondo H., Anazawa H., Terasaki Y.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB022700; BAA74433.1; -
 DR HSP; P34752; 1IHP.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.

DR InterPro; IPR000560; HisAc phsptse.
 DR Pfam; PF00328; Acid phosphat A; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 SQ SEQUENCE 467 AA; 51028 MW; 7A38AD543EDC265C CRC64;

 Query Match 96.6%; Score 2278; DB 2; Length 467;
 Best Local Similarity 95.3%; Pred. No. 1.7e-161;
 Matches 427; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

 Qy 2 LAVPASRNQSSCDTVDQGYQCFSTSHLWGQYAPFFSLANESVTSPEVPAGCRVTFPAQVL 61
 Db 20 LAVPASRNQSSCDTVDQGYQCFSTSHLWGQYAPFFSLANESVTSPEVPAGCHVTFPAQVL 79

 Qy 62 SRHGARYPTDSKGKYSALIBEIQQNATTFPGKYAFKTKYNSLGADDLTPFGQELVNS 121
 Db 80 SRHGARYPTDSKGKYSALIBEIQQNATTFPGKYAFKTKYNSLGADDLTPFGQELVNS 139

 Qy 122 GIKFYQRYESLTRNIVPFIRSSGSRVIAAGKKEIEGFQSTKLDRAQPGQSSPKIDVV 181
 Db 140 GIKFYQRYESLTRNIVPFIRSSGSRVIAAGKKEIEGFQSTKLDRAQPGQSSPKIDVV 199

 Qy 182 ISEASSNNITDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVLTDTEVY 241
 Db 200 ISEASTNNITDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVLTDTEVY 259

 Qy 242 LMDMCSFDTTSTVDTKLSFPCDLFTHDEWINVDYLQSLKYYGHGAGNPLGPTQGVY 301
 Db 260 LMDMCSFDTTSTVDTKLSFPCDLFTHDEWINVDYLQSLKYYGHGAGNPLGPTQGVY 319

 Qy 302 ANELIARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSDHNGIISILFALGLYNGTK 361
 Db 320 ANELIARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSDHNGIISILFALGLYNGTK 379

 Qy 362 PLSTTTVENTITQDTGFSSAWTVFPASRLYVEMMQCQAEPLVRVLVNDRVVPLHGCPVD 421
 Db 380 PLSTTTAENITQDTGFSSAWTVFPASRLYVEMMQCQAEPLVRVLVNDRVVPLHGCPVD 439

 Qy 422 ALGRCRDSFVRGLSFARSGGDWAECEFA 449
 Db 440 ALGRCRDSFVRGLSFARSGGDWAECEFA 467

 RESULT 10
 O6GYA8 PRELIMINARY; PRT; 448 AA.
 AC O6GYA8
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DE Phytase (Fragment).
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Aspergillus.
 OX NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N-2;
 RA Wu J., Yan C.Y.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY615712; AAT51735.1; -
 DR InterPro; IPR000560; HisAc phsptse.
 DR Pfam; PF00328; Acid phosphat A; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase.
 FT NON TER 1
 SQ SEQUENCE 448 AA; 49170 MW; C319E1FECB4EF18 CRC64;

 Query Match 96.4%; Score 2273; DB 2; Length 448;
 Best Local Similarity 95.1%; Pred. No. 3.8e-161;
 Matches 426; Conservative 15; Mismatches 7; Indels 0; Gaps 0;

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QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPVEPAGCRVTFQAQVL 61
Db 1 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANKSAISPDVPAGCHVTFQAQVL 60
QY 62 SRHGARYPTDSKGKYSALIEIQNATTFDQGYAFLKTYNYSLGADDLTPFGEQELVNS 121
Db 61 SRHGARYPTDSKGKYSALIEIQNATTFEKGYAFLKTYNYSLGADDLTPFGEQELVNS 120
QY 122 GIKFYQRYESLTRNIVPFIRSSGSRVIAASGNKFTIEGQSTKLKDPRAQPGQSSPKIDVV 181
Db 121 GIKFYQRYESLTRNIVPFIRSSGSRVIAASGNKFTIEGQSTKLKDPRAQPGQSSPKIDVV 180
QY 182 ISEASSNNITDPGCTVFEDSELADTVEANFTATFVPSIRORLENDISGVTLTTEVTY 241
Db 181 ISEASTSNITDPGCTVFEDSELADTVEANFTATFVPSIRORLENDISGVSLTTEVTY 240
QY 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYKGAGNPLGPTQGVGY 301
Db 241 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYKGAGNPLGPTQGVGY 300
QY 302 ANELIARLTHSPVHDDTSSNHTLDSNPATFPPLNSTLYADFSDHNGIISILFALGLYNGTK 361
Db 301 ANELIARLTHSPVHDDTSSNHTLDSNPATFPPLNSTLYADFSDHNGIISILFALGLYNGTK 360
QY 362 PLSTTTVENITQTDGFSASWTVPFASRLYVENMQCAEQEPLRVLRVLRVNDRVVPLHGCPVD 421
Db 361 PLSTTTAENITQTDGFSASWTVPFASRLYVENMQCAEQEPLRVLRVLRVNDRVVPLHGCPVD 420
QY 422 ALGRCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 421 ALGRCRTRDSFVKGLSFARSGGDWAECEFA 448

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RESULT 11
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 ID Q9HEQ0 PRELIMINARY; PRT; 467 AA.
 AC Q9HEQ0;
 DT 01-VAR-2001 (TremBLrel. 16, Created)
 DT 01-VAR-2001 (TremBLrel. 16, Last sequence update)
 DT 01-VAR-2004 (TremBLrel. 26, Last annotation update)
 DE Phytase.
 OS Aspergillus ficum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5058;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang L., An L., Wang Y., Yuan X.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY013315; AAG4085.1; -.
 DR HSP; P34752; IHP.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro; IPR000560; HisAc_phsphtse.
 DR Pfam; PF00328; Acid_phosphat_A; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 SQ SEQUENCE 467 AA; 51012 MW; 3F69AD543C0B565B CRC64;

Query Match 96.2%; Score 2268; DB 2; Length 467;
 Best Local Similarity 95.3%; Pred. No. 9.4e-161;
 Matches 427; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

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QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPVEPAGCRVTFQAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANKSAISPDVPAGCHVTFQAQVL 79
QY 62 SRHGARYPTDSKGKYSALIEIQNATTFDQGYAFLKTYNYSLGADDLTPFGEQELVNS 121
Db 80 SRHGARYPTDSKGKYSALIEIQNATTFEKGYAFLKTYNYSLGADDLTPFGEQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFIRSSGSRVIAASGNKFTIEGQSTKLKDPRAQPGQSSPKIDVV 181

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Db 140 GVKFYQRYESLTRNIVPFIRSSGSRVIAASGNKFTIEGQSTKLKDPRAQPGQSSPKIDVV 199
QY 182 ISEASSNNITDPGCTVFEDSELADTVEANFTATFVPSIRORLENDISGVTLTTEVTY 241
Db 200 ISEASTSNITDPGCTVFEDSELADTVEANFTATFVPSIRORLENDISGVSLTTEVTY 259
QY 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYKGAGNPLGPTQGVGY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYKGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSNPATFPPLNSTLYADFSDHNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSNPATFPPLNSTLYADFSDHNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSASWTVPFASRLYVENMQCAEQEPLRVLRVLRVNDRVVPLHGCPVD 421
Db 380 PLSTTTAENITQTDGFSASWTVPFASRLYVENMQCAEQEPLRVLRVLRVNDRVVPLHGCPVD 439
QY 422 ALGRCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGRCRTRDSFVKGLSFARSGGDWAECEFA 467

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RESULT 12
 Q6R519
 ID Q6R519 PRELIMINARY; PRT; 467 AA.
 AC Q6R519;
 DT 05-JUL-2004 (TremBLrel. 27, Created)
 DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
 DE Phytase A.
 GN Name=phyA;
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Wu Y., Che C.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY513749; AAS00648.1; -.
 DR InterPro; IPR000560; HisAc_phsphtse.
 DR Pfam; PF00328; Acid_phosphat_A; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 SQ SEQUENCE 467 AA; 51094 MW; 64AD065AB27AC099 CRC64;

Query Match 96.1%; Score 2265; DB 2; Length 467;
 Best Local Similarity 95.1%; Pred. No. 1.6e-160;
 Matches 426; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

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QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPVEPAGCRVTFQAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLAQSIVISPDVPAGCRVTFQAQVL 79
QY 62 SRHGARYPTDSKGKYSALIEIQNATTFDQGYAFLKTYNYSLGADDLTPFGEQELVNS 121
Db 80 SRHGARYPTDSKGKYSALIEIQNATTFDQGYAFLKTYNYSLGADDLTPFGEQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFIRSSGSRVIAASGNKFTIEGQSTKLKDPRAQPGQSSPKIDVV 181
Db 140 GIKFYQRYESLTRNIVPFIRSSGSRVIAASGNKFTIEGQSTKLKDPRAQPGQSSPKIDVV 199
QY 182 ISEASSNNITDPGCTVFEDSELADTVEANFTATFVPSIRORLENDISGVTLTTEVTY 241
Db 200 ISEASTSNITDPGCTVFEDSELADTVEANFTATFVPSIRORLENDISGVSLTTEVTY 259
QY 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYKGAGNPLGPTQGVGY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYKGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSNPATFPPLNSTLYADFSDHNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSNPATFPPLNSTLYADFSDHNGIISILFALGLYNGTK 379

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QY	362	PLSTTTIVENTQTDDGFSAAWTPFASRLYVEMMQCAEQEPLVRVLVNDVRVPLHGCPVD	421
Db	380	PLSTTTTAENITQTDGFSAAWTPFASRLYVEMMQCAENEPLVRVLVNDVRVPLHGCPAD	439
QY	422	ALGRCRTDSSFVRGLSFARSGGDWAECA	449
Db	440	ALGRCRTDSSFVRGLSFARSGGDWAECA	467

RESULT 13

AA000648	PRELIMINARY;	PRT;	467 AA.
ID	AA000648		
AC	AA000648;		
DT	C2-MAR-2004	(TrEMBLrel. 27, Created)	
DT	C2-MAR-2004	(TrEMBLrel. 27, Last sequence update)	
DT	C2-MAR-2004	(TrEMBLrel. 27, Last annotation update)	
DE	Phytase A.		
GN	PHYA.		
OS	Aspergillus niger.		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;		
OC	Euriales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.		
OX	NCBI_TaxID=5061;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Zhang Y., Wu Y., Che C.;		
RT	"Aspergillus niger phytase.;"		
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY513749; AA000648.1; -		
SQ	SEQUENCE 467 AA; 51094 MW; 64AD06BA827AC099	CRC64;	

Db 80 RHGARYPTSSKSKYKLVLTATQANATDFKGFALFKTYNYTLGADLLTPFGEOQLVNSG 139
QY 123 IKFYQRYESLRNIVPFIIRSSGSSRVIASGKFFIEGFQSTKLKDPRAQPGQSSPKIDVVI 182
Db 140 IKFYQRYKALARSVVFFIRASGSDRVIASGKFFIEGFQOAKUADPGA-TNRAAPAIsvII 198
QY 183 SEASSNNTLPDGTCTVPEFSDSLADTVANFTATVPFSIRQRLNDLSGVTLTDEVTYL 242
Db 199 PESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIRABAEKHLPGVTLTDEDVVS 258
QY 243 MDMCFDTISTSTVTKLSPPFCDLTFHDEWINYDLSKLYKYGAGNPLGPTQGVGYA 302
Db 259 MDMCFDTVARTSDASQLSPFCQLFTHEWKKNYLQSLGKYGYGAGNPLGPAQGI 318
QY 303 NELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKP 362
Db 319 NELIARLTHSPVQDHTSINSTLVSPATFPLNSTLYADFSHDNSMVSIFFAUGLNGTEP 378
QY 363 LSTTVENITQTDGFSSAWTPFASRLYVEMMQCAOEPLVRLVNDRVPLHGCVPVDA 422
Db 379 LSRTSVESAKELDGYASWVVPFARAYFETWQCKSEKEFLVRLALINDRVVPLHGCVDK 438
QY 423 LGRCTRDSFVRGLSFARSGGDWAECEFA 449
Db 439 LGRCKLNDVFKLSWARSNGNWGECFS 465

RESULT 15

Q9C1T1 PRELIMINARY; PRT; 466 AA.
AC Q9C1T1; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phycase.
GN Name=phyA;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RA Gomi K.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB042805; BAB40715.1; -.
DR HSSP; P34752; 1IHP.
DR GO; GO:0003993; P:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN 1.
SQ SEQUENCE 466 AA, 51257 MW, 8033BED57FBA2791 CRC64;

Query Match 68.3%; Score 1610; DB 2; Length 466;
Best Local Similarity 67.0%; Pred. No. 1.3e-111;
Matches 297; Conservative 57; Mismatches 89; Indels 0; Gaps 0;
QY 7 SRNOSCDTVDOGYQCFSTSLWGQYAPFSLANESVISPVPAGCRVTFPAQLSRHGA 66
Db 24 SPQQSCNTVDGYQCFSGVSLWGQYSPFYSDDESSLSDVPDHCQVTFPAQLSRHGA 83
QY 67 RYPTDSKGYKYSALIEICQNAFTPDGKVAFLKTYNYSIGADLLTPFGBOELVNSGIKEY 126
Db 84 RYPTKSKSEYAKLKVQHNATSFSGKYAFLKSYNYSIGADLLTPFGENQLVDSGIKEY 143
QY 127 QRYESLTRNIVPFIIRSSGSSRVIASGKFFIEGFQSTKLKDPRAQPGQSSPKIDVWIS 186
Db 144 QRYEELAKNVVPIFIRASGSDRVIASGKFFIEGFQKAKLGDSKSKRGQAPIVNVVITETE 203
QY 187 SSNTLDPGTCTVPESESLADTVANFTATVPFSIRQRLNDLSGVTLTDEVTYIMDMC 246
Db 204 GFNNTLDHSLCTAFENSTTGDAEDKFTAVFTVPSIVERLEKDLPGTTLSSKEVYIMDMC 263

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Job time : 139 secs

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Db 264 SFDIATLRTDGSRLSPFCALFTQBEWAQYDYLSQSVSKYGYGGNPLGPAQOIGFANELI 323
QY 307 ARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTT 366
Db 324 ARLTKSPVKDHTTNTTLDSPATFPLNATLYADFSHDNTMTSVFFALGLYNTTPELSQT 383
QY 367 TVENITQTDGFSSAWTPFASRLYVEMMQCAOEPLVRLVNDRVPLHGCVPVDA 426
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QY 427 TRDSFVRGLSFARSGGDWAECEFA 449
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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 24, 2004, 11:28:49 ; Search time 54 Seconds
(without alignments)
551.422 Million cell updates/sec

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Perfect score: 2358
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/protdata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/protdata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/protdata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2353	99.8	467	1 US-08-151-574-32	Sequence 32, Appl
2	2353	99.8	467	1 US-08-146-424-20	Sequence 20, Appl
3	2353	99.8	467	1 US-08-693-709-2	Sequence 2, Appl
4	2353	99.8	467	2 US-08-419-448-32	Sequence 32, Appl
5	2353	99.8	467	2 US-08-819-825-3	Sequence 3, Appl
6	2353	99.8	467	3 US-09-163-642-3	Sequence 3, Appl
7	2353	99.8	467	3 US-09-233-510-32	Sequence 32, Appl
8	2353	99.8	467	4 US-09-636-499-5	Sequence 5, Appl
9	2341	99.3	467	4 US-09-273-871A-11	Sequence 11, Appl
10	2341	99.3	467	4 US-10-083-452-11	Sequence 11, Appl
11	2334	99.0	444	3 US-09-044-718-1	Sequence 1, Appl
12	2334	99.0	444	4 US-10-062-848-1	Sequence 1, Appl
13	2321	98.4	441	4 US-09-684-855-105	Sequence 105, Appl
14	2321	98.4	441	4 US-09-684-855-127	Sequence 127, Appl
15	2321	98.4	441	4 US-09-684-855-150	Sequence 150, Appl
16	2321	98.4	441	4 US-09-684-855-149	Sequence 5, Appl
17	2321	98.4	462	4 US-09-636-499-12	Sequence 12, Appl
18	2309	97.9	467	1 US-07-923-724-8	Sequence 8, Appl
19	2309	97.9	467	2 US-08-609-426A-8	Sequence 8, Appl
20	2309	97.9	467	2 US-08-374-652C-2	Sequence 2, Appl
21	2288	97.0	441	4 US-09-684-855-104	Sequence 104, Appl
22	2288	97.0	441	4 US-09-684-855-149	Sequence 149, Appl
23	2288	97.0	441	4 US-09-488-265B-4	Sequence 4, Appl
24	2278	96.6	467	3 US-09-155-855-3	Sequence 3, Appl
25	2278	96.6	467	3 US-09-543-744-3	Sequence 3, Appl
26	2278	96.6	467	3 US-09-929-060-3	Sequence 3, Appl
27	2277	96.6	441	4 US-09-684-855-103	Sequence 103, Appl

28	2277	96.6	441	4 US-09-684-855-126	Sequence 126, Appl
29	2277	96.6	441	4 US-09-684-855-148	Sequence 148, Appl
30	2277	96.6	441	4 US-09-488-265B-3	Sequence 3, Appl
31	2255	95.6	443	3 US-09-155-855-1	Sequence 1, Appl
32	2255	95.6	443	3 US-09-543-744-1	Sequence 1, Appl
33	2255	95.6	443	4 US-09-929-060-1	Sequence 1, Appl
34	2242	95.1	443	3 US-09-155-855-2	Sequence 2, Appl
35	2242	95.1	443	3 US-09-543-744-2	Sequence 2, Appl
36	2242	95.1	443	4 US-09-929-060-2	Sequence 2, Appl
37	1990	84.4	410	4 US-09-636-499-11	Sequence 11, Appl
38	1932	81.9	467	4 US-09-684-855-167	Sequence 167, Appl
39	1929	81.8	467	4 US-09-488-265B-35	Sequence 35, Appl
40	1833	77.7	467	4 US-09-684-855-161	Sequence 161, Appl
41	1833	77.7	467	4 US-09-488-265B-29	Sequence 29, Appl
42	1828	77.5	467	4 US-09-488-265B-91	Sequence 91, Appl
43	1822	77.3	467	4 US-09-488-265B-93	Sequence 93, Appl
44	1820	77.2	441	4 US-09-488-265B-24	Sequence 24, Appl
45	1820	77.2	467	4 US-09-684-855-139	Sequence 139, Appl

ALIGNMENTS

RESULT 1
US-08-151-574-32
; Sequence 32, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Seltin
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-151-574-32

Query Match 99.8%; Score 2353; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 9e-235;


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Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LAVPASNQSCDVTDOGYQCFSETSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 61
Db 20 LAVPASNQSCDVTDOGYQCFSETSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEEQONATTDFGKYAFKTYNYSLGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGGKYSALIEEQONATTDFGKYAFKTYNYSLGADDLTPFGQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKDPRAQPCQSSPKIDVV 181
Db 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKDPRAQPCQSSPKIDVV 199
QY 182 ISRASSNNLTDPGCTVFPEDSELADTVANFTATFVPSIRORLENDLSGVTLLDTEVTY 241
Db 200 ISRASSNNLTDPGCTVFPEDSELADTVANFTATFVPSIRORLENDLSGVTLLDTEVTY 259
QY 242 LDMCSPDFTISTSTVDTKLSPPFCDLFTHDEWINYDYLQSLKKYXGAGNPLGPTQGVGY 301
Db 260 LDMCSPDFTISTSTVDTKLSPPFCDLFTHDEWINYDYLQSLKKYXGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDS SPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDS SPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRVLNDRVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRVLNDRVPLHGCPVD 439
QY 422 ALGRCRTDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGRCRTDSFVRGLSFARSGGDWAECEFA 467

RESULT 2
US-08-146-424-20
; Sequence 20, Application US/08146424
; Patent No. 5593963
; GENERAL INFORMATION:
; APPLICANT: VAN OOIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/DOCKET NUMBER: 44615-20011.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 20:

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LAVPASNQSCDVTDOGYQCFSETSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 61
Db 20 LAVPASNQSCDVTDOGYQCFSETSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEEQONATTDFGKYAFKTYNYSLGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGGKYSALIEEQONATTDFGKYAFKTYNYSLGADDLTPFGQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKDPRAQPCQSSPKIDVV 181
Db 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKDPRAQPCQSSPKIDVV 199
QY 182 ISRASSNNLTDPGCTVFPEDSELADTVANFTATFVPSIRORLENDLSGVTLLDTEVTY 241
Db 200 ISRASSNNLTDPGCTVFPEDSELADTVANFTATFVPSIRORLENDLSGVTLLDTEVTY 259
QY 242 LDMCSPDFTISTSTVDTKLSPPFCDLFTHDEWINYDYLQSLKKYXGAGNPLGPTQGVGY 301
Db 260 LDMCSPDFTISTSTVDTKLSPPFCDLFTHDEWINYDYLQSLKKYXGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDS SPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDS SPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRVLNDRVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRVLNDRVPLHGCPVD 439
QY 422 ALGRCRTDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGRCRTDSFVRGLSFARSGGDWAECEFA 467

SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-146-424-20
Query Match 99.8%; Score 2353; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 9e-235;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LAVPASNQSCDVTDOGYQCFSETSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 61
Db 20 LAVPASNQSCDVTDOGYQCFSETSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEEQONATTDFGKYAFKTYNYSLGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGGKYSALIEEQONATTDFGKYAFKTYNYSLGADDLTPFGQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKDPRAQPCQSSPKIDVV 181
Db 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKDPRAQPCQSSPKIDVV 199
QY 182 ISRASSNNLTDPGCTVFPEDSELADTVANFTATFVPSIRORLENDLSGVTLLDTEVTY 241
Db 200 ISRASSNNLTDPGCTVFPEDSELADTVANFTATFVPSIRORLENDLSGVTLLDTEVTY 259
QY 242 LDMCSPDFTISTSTVDTKLSPPFCDLFTHDEWINYDYLQSLKKYXGAGNPLGPTQGVGY 301
Db 260 LDMCSPDFTISTSTVDTKLSPPFCDLFTHDEWINYDYLQSLKKYXGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDS SPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDS SPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRVLNDRVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRVLNDRVPLHGCPVD 439
QY 422 ALGRCRTDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGRCRTDSFVRGLSFARSGGDWAECEFA 467

RESULT 3
US-08-693-709-2
; Sequence 2, Application US/08693709
; Patent No. 5779413
; GENERAL INFORMATION:
; APPLICANT: VAN OOIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IEM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,709
; FILING DATE: 07-AUG-1996
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; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,424
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20011.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...23
; OTHER INFORMATION:
;
; US-08-693-709--2
;
; Query Match 99.8%; Score 2353; DB 1; Length 467;
; Best Local Similarity 100.0%; Pred. No. 9e-235;
; Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 2 LVPASRNQSSCDTVDQGYQCFSTSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQL 61
Db 20 LVPASRNQSSCDTVDQGYQCFSTSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQL 79
QY 62 SRHGARYPTDSKGKYYGALLIEEQONATTFDGKYAFI.KTNYNSLGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGKYYGALLIEEQONATTFDGKYAFI.KTNYNSLGADDLTPFGQELVNS 139
QY 122 GIKFYQYESLTRNIVPFISSGSSRVIASGKFIIEGFQSTKLKDPRAQPGQSSPKIDVV 181
Db 140 GIKFYQYESLTRNIVPFISSGSSRVIASGKFIIEGFQSTKLKDPRAQPGQSSPKIDVV 199
QY 182 ISEASSNNLTDPGCTCFVFEDELADTVEANFTATFVPSIRQLENLDSGVTLTDEVTY 241
Db 200 ISEASSNNLTDPGCTCFVFEDELADTVEANFTATFVPSIRQLENLDSGVTLTDEVTY 259
QY 242 LMDMCSFDTTSTSTVDTKLSPFCDFLTHDEWINTDYQLSKKKYGHGAGNPLGTQGVGY 301
Db 260 LMDMCSFDTTSTSTVDTKLSPFCDFLTHDEWINTDYQLSKKKYGHGAGNPLGTQGVGY 319
QY 302 ANELIARLTSPVHDDTSSNHTLTDSSPATPELNSTLYADFSHDNGIISILFALGIYNGTK 361
Db 320 ANELIARLTSPVHDDTSSNHTLTDSSPATPELNSTLYADFSHDNGIISILFALGIYNGTK 379
QY 362 PLSTTTTVENTITQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPLHGCPVD 421
Db 380 PLSTTTTVENTITQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPLHGCPVD 439
QY 422 ALGCTRDSFVRGLSFARSGDWAECTA 449
Db 440 ALGCTRDSFVRGLSFARSGDWAECTA 467

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Qy	362	PLSTTTVENTITQTDGSSAWTVFPASLKYEMMQCAEQEPLVRLVNDRVVPLHGC	421
Db	380	PLSTTTVENTITQTDGSSAWTVFPASLKYEMMQCAEQEPLVRLVNDRVVPLHGC	439
Qy	422	ALGCRTRDSFVRGLSFARSGGDWAECFA	449
Db	440	ALGCRTRDSFVRGLSFARSGGDWAECFA	467

RESULT 5

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US-08-819-825-3
; Sequence 3, Application US/08819825
; Patent No. 5866118
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Ray, Michael W.
; APPLICANT: Klotz, Alan V.
; TITLE OF INVENTION: Polypeptides Having Phytase Activity
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,825
; FILING DATE: 18-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4758.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-819-825-3
Query Match 99.8%; Score 2353; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 9e-235;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSCDVTDOGYQCFSETSHLWGQYAPFFPSLANESVISPVPAGCRVTFQAVL 61
DB 20 LAVPASRNQSCDVTDOGYQCFSETSHLWGQYAPFFPSLANESVISPVPAGCRVTFQAVL 79
QY 62 SRHGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNSLGLADDLTPFGEQELVNS 121
DB 80 SRHGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNSLGLADDLTPFGEQELVNS 139
QY 122 GIKFYQRYESLNRNIVPFRSSGSSRVIASGKPIEGFQSTKLKDPRAQPGQSSPKIDVV 181
DB 140 GIKFYQRYESLNRNIVPFRSSGSSRVIASGKPIEGFQSTKLKDPRAQPGQSSPKIDVV 199
QY 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVY 241
DB 200 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVY 259
QY 242 LMDMCSFDTTISTVTDKLSPFCDLFTHDEWINVDYLSLKKYKGAGNPLGPTQGVY 301
DB 260 LMDMCSFDTTISTVTDKLSPFCDLFTHDEWINVDYLSLKKYKGAGNPLGPTQGVY 319

US-09-163-642-3
; Sequence 3, Application US/09163642
; Patent No. 6221644
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Ray, Michael W.
; APPLICANT: Klotz, Alan V.
; TITLE OF INVENTION: Polypeptides Having Phytase Activity
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6221644o No. 6221644disk of No. 6221644th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/163,642
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,825
; FILING DATE: 18-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4758.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-163-642-3
Query Match 99.8%; Score 2353; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 9e-235;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSCDVTDOGYQCFSETSHLWGQYAPFFPSLANESVISPVPAGCRVTFQAVL 61
DB 20 LAVPASRNQSCDVTDOGYQCFSETSHLWGQYAPFFPSLANESVISPVPAGCRVTFQAVL 79
QY 62 SRHGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNSLGLADDLTPFGEQELVNS 121
DB 80 SRHGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNSLGLADDLTPFGEQELVNS 139
QY 122 GIKFYQRYESLNRNIVPFRSSGSSRVIASGKPIEGFQSTKLKDPRAQPGQSSPKIDVV 181
DB 140 GIKFYQRYESLNRNIVPFRSSGSSRVIASGKPIEGFQSTKLKDPRAQPGQSSPKIDVV 199
QY 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVY 241
DB 200 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVY 259
QY 242 LMDMCSFDTTISTVTDKLSPFCDLFTHDEWINVDYLSLKKYKGAGNPLGPTQGVY 301
DB 260 LMDMCSFDTTISTVTDKLSPFCDLFTHDEWINVDYLSLKKYKGAGNPLGPTQGVY 319
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Qy	302	ANELIARLTSPVHDDTSNHTLSSPATFPPLNSTLYADFSDNDGIIISILFALGHYNGTK	361
Db	320	ANELIARLTSPVHDDTSNHTLSSPATFPPLNSTLYADFSDNDGIIISILFALGHYNGTK	379
Qy	362	PLSTTTVENTITQDTGFSASWTPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD	421
Db	380	PLSTTTVENTITQDTGFSASWTPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD	439
Qy	422	ALGCTRDSFVRGLSFARSGGDWAECPA	449
Db	440	ALGCTRDSFVRGLSFARSGGDWAECPA	467

RESIT.T 7

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US-09-233-510-32
/ Sequence 32, Application US/092333510
/ Patent No. 6350602
/ GENERAL INFORMATION:
/ APPLICANT: Robert F.M. Van Gorcom
/ APPLICANT: Willem Van Hartingsveldt
/ APPLICANT: Petrus A. Van Paridon
/ APPLICANT: Annemarie E. Veenstra
/ APPLICANT: Rudolf G.M. Luttin
/ APPLICANT: Gerardus Seiten
/ TITLE OF INVENTION: Cloning and Expression of Microbial
/ TITLE OF INVENTION: Phytase
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Morrison & Foerster
/ STREET: 545 Middlefield Road, Suite 200
/ CITY: Menlo Park
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94025-3471
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/233,510
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/688,578
/ FILING DATE: 24-MAY-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Murashige, Kate H.
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 24615-20026.00
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-327-7250
/ TELEFAX: 415-327-2951
/ INFORMATION FOR SEQ ID NO: 32:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 467 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-233-510-32

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Db      80  SRGARYPTDSKGGKYSALIEBIQQNATTFDGKYAFKTYNYSGLGADDLTPFGEQELVNS  139
QY      122  GIKFYQRYESLTENIVPFIIRSSGSSRVIASGKKFIEGFQSTKLKPRAQPGQSSPKIDVV  181
Db      140  GIKFYQRYESLTENIVPFIIRSSGSSRVIASGKKFIEGFQSTKLKPRAQPGQSSPKIDVV  199
QY      182  ISASSSNNITLDGCTCTVFEDSLADTVANFATFVPSIRQBLENDLSGVTITDTEVTY  241
Db      200  ISEASSNNITLDGCTCTVFEDSLADTVANFATFVPSIRQBLENDLSGVTITDTEVTY  259
QY      242  LMDWCSFDITSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGY  301
Db      260  LMDWCSFDITSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGY  319
QY      302  ANELIARLTHSPVHDDTSSNHTLDSSEPAFPLNSTLYADPSHDNGIISILFALGLYNGTK  361
Db      320  ANELIARLTHSPVHDDTSSNHTLDSSEPAFPLNSTLYADPSHDNGIISILFALGLYNGTK  379
QY      362  PLSTTTVENITQDGFSSAWTVFASRLYVEMMQCAQEPLVRVLVNDRVVPLHGCPCVD  421
Db      380  PLSTTTVENITQDGFSSAWTVFASRLYVEMMQCAQEPLVRVLVNDRVVPLHGCPCVD  439
QY      422  ALGCRTRDSFVRGLSFARSGGDWAECFA  449
Db      440  ALGCRTRDSFVRGLSFARSGGDWAECFA  467

RESULT 8
US-09-636-499-5
; Sequence 5, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCES: GC586-2
; CURRENT APPLICATION NUMBER: US/09/636,499
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRN
; ORGANISM: Aspergillus niger
; US-09-636-499-5

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RESULT 8

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US-09-636-499-5
; Sequence 5, Application US/09636499
; Patent No. 6475762
;
GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
;
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC986-2
;
CURRENT APPLICATION NUMBER: US/09/636,499
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/148,960
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
;
US-09-636-499-5

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QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 421
DB 380 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 439
QY 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
DB 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 9
US-09-273-871A-11
; Sequence 11, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273.871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus ficum
US-09-273-871A-11

Query Match 99.3%; Score 2341; DB 4; Length 467;
Best Local Similarity 99.6%; Pred. No. 1.6e-233;
Matches 446; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGOYAPFFPSLANESVISPEVPAGCRVTFAQVL 61
DB 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGOYAPFFPSLANESVISPEVPAGCRVTFAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNYSLGADDLTPFGQEQLVNS 121
DB 80 SRHGARYPTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNYSLGADDLTPFGQEQLVNS 139
QY 122 GIKFYQYESTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDPRAQCGQSSPKIDVV 181
DB 140 GIKFYQYESTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDPRAQCGQSSPKIDVV 199
QY 182 ISBASSNNLTDPGCTCTVFEDSELADTVANFTATFVPSIRQRIENLDSGLVTLTDEVTY 241
DB 200 ISBASSNNLTDPGCTCTVFEDSELADTVANFTATFVPSIRQRIENLDSGLVTLTDEVTY 259
QY 242 LMDWCSPDTTSTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYCHGAGNPLGPTQGVY 301
DB 260 LMDWCSPDTTSTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYCHGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 421
DB 380 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 439
QY 362 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 421

DB 380 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 439
QY 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
DB 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467
RESULT 10
US-10-083-452-11
; Sequence 11, Application US/10083452
; Patent No. 6689358
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083.452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273.871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus ficum
US-10-083-452-11

Query Match 99.3%; Score 2341; DB 4; Length 467;
Best Local Similarity 99.6%; Pred. No. 1.6e-233;
Matches 446; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGOYAPFFPSLANESVISPEVPAGCRVTFAQVL 61
DB 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGOYAPFFPSLANESVISPEVPAGCRVTFAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNYSLGADDLTPFGQEQLVNS 121
DB 80 SRHGARYPTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNYSLGADDLTPFGQEQLVNS 139
QY 122 GIKFYQYESTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDPRAQCGQSSPKIDVV 181
DB 140 GIKFYQYESTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDPRAQCGQSSPKIDVV 199
QY 182 ISBASSNNLTDPGCTCTVFEDSELADTVANFTATFVPSIRQRIENLDSGLVTLTDEVTY 241
DB 200 ISBASSNNLTDPGCTCTVFEDSELADTVANFTATFVPSIRQRIENLDSGLVTLTDEVTY 259
QY 242 LMDWCSPDTTSTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYCHGAGNPLGPTQGVY 301
DB 260 LMDWCSPDTTSTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYCHGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 421
DB 380 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 439
QY 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449

Db 440 ALGCRTRDSFVRGLSFARSGGDWAECA 467
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RESULT 11

US-09-044-718-1
; Sequence 1, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-044-718-1

Query Match 99.0%; Score 2334; DB 3; Length 444;
Best Local Similarity 100.0%; Pred. No. 7.7e-233;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ASRNQSCDVTDDQGYQCFSETSHLWQYAPFSLANESVISPEVAGCRVTPAQVLSRHG 65
Db 1 ASRNQSCDVTDDQGYQCFSETSHLWQYAPFSLANESVISPEVAGCRVTPAQVLSRHG 60
QY 66 ARYPTDSKGGKYSALIEIEIQNATTFDGKYAFKTYNYSGLGADDLTPFGEQELVNSGKIF 125
Db 61 ARYPTDSKGGKYSALIEIEIQNATTFDGKYAFKTYNYSGLGADDLTPFGEQELVNSGKIF 120
QY 126 YQRYESLNRNIVPFRSSGSRVIAAGKFFIEGFQSTKLDPRAQPGQSSPKIDVWVISEA 185
Db 121 YQRYESLNRNIVPFRSSGSRVIAAGKFFIEGFQSTKLDPRAQPGQSSPKIDVWVISEA 180
QY 186 SSSNNTLDPGCTVDFEDSELADTVEANFTATVPFSIRQRLNDLSGVTLTDTTEVTYLMDM 245
Db 181 SSSNNTLDPGCTVDFEDSELADTVEANFTATVPFSIRQRLNDLSGVTLTDTTEVTYLMDM 240
QY 246 CSFDTISTSTVDTKLSPPCDLTFHDEWINYDLSLKKYKGAGNPLGPTQGVGYANEL 305
Db 241 CSFDTISTSTVDTKLSPPCDLTFHDEWINYDLSLKKYKGAGNPLGPTQGVGYANEL 300
QY 306 IARLTHSPVHDDTSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 365
Db 301 IARLTHSPVHDDTSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
QY 366 TTVENITQDGFSSAWTVPFASRLYVENMQCOAEQELVRLVNDRVVPLHGPCVDALGR 425
Db 361 TTVENITQDGFSSAWTVPFASRLYVENMQCOAEQELVRLVNDRVVPLHGPCVDALGR 420
QY 426 CTRDSFVRGLSFARSGGDWAECA 449
Db 421 CTRDSFVRGLSFARSGGDWAECA 444

RESULT 12

US-10-062-848-1
; Sequence 1, Application US/10062848
; Patent No. 6734004
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis

; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-062-848-1

Query Match 99.0%; Score 2334; DB 4; Length 444;
Best Local Similarity 100.0%; Pred. No. 7.7e-233;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ASRNQSCDVTDDQGYQCFSETSHLWQYAPFSLANESVISPEVAGCRVTPAQVLSRHG 65
Db 1 ASRNQSCDVTDDQGYQCFSETSHLWQYAPFSLANESVISPEVAGCRVTPAQVLSRHG 60
QY 66 ARYPTDSKGGKYSALIEIEIQNATTFDGKYAFKTYNYSGLGADDLTPFGEQELVNSGKIF 125
Db 61 ARYPTDSKGGKYSALIEIEIQNATTFDGKYAFKTYNYSGLGADDLTPFGEQELVNSGKIF 120
QY 126 YQRYESLNRNIVPFRSSGSRVIAAGKFFIEGFQSTKLDPRAQPGQSSPKIDVWVISEA 185
Db 121 YQRYESLNRNIVPFRSSGSRVIAAGKFFIEGFQSTKLDPRAQPGQSSPKIDVWVISEA 180
QY 186 SSSNNTLDPGCTVDFEDSELADTVEANFTATVPFSIRQRLNDLSGVTLTDTTEVTYLMDM 245
Db 181 SSSNNTLDPGCTVDFEDSELADTVEANFTATVPFSIRQRLNDLSGVTLTDTTEVTYLMDM 240
QY 246 CSFDTISTSTVDTKLSPPCDLTFHDEWINYDLSLKKYKGAGNPLGPTQGVGYANEL 305
Db 241 CSFDTISTSTVDTKLSPPCDLTFHDEWINYDLSLKKYKGAGNPLGPTQGVGYANEL 300
QY 306 IARLTHSPVHDDTSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 365
Db 301 IARLTHSPVHDDTSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
QY 366 TTVENITQDGFSSAWTVPFASRLYVENMQCOAEQELVRLVNDRVVPLHGPCVDALGR 425
Db 361 TTVENITQDGFSSAWTVPFASRLYVENMQCOAEQELVRLVNDRVVPLHGPCVDALGR 420
QY 426 CTRDSFVRGLSFARSGGDWAECA 449
Db 421 CTRDSFVRGLSFARSGGDWAECA 444

RESULT 13

US-09-684-855-105
; Sequence 105, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 105
; LENGTH: 441
; TYPE: PRT
; ORGANISM: A. niger NRRL3135
; US-09-684-855-105

Query Match          98.4%; Score 2321; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.7e-231;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  9  NQSSCDTVDOGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARY 68
Db  1  NQSSCDTVDOGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARY 60

Qy  69  PTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSIGADDLTPFGQELVNSGKIFYOR 128
Db  61  PTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSIGADDLTPFGQELVNSGKIFYOR 120

Qy  129  YESLTRNIVPFISSGSSSRVIAAGKKEIEGFQSTKLKDPRAQPGQSSPKIDVVISEASS 188
Db  121  YESLTRNIVPFISSGSSSRVIAAGKKEIEGFQSTKLKDPRAQPGQSSPKIDVVISEASS 180

Qy  189  NNTLDPGCTCTVFDESELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVYLMDCSF 248
Db  181  NNTLDPGCTCTVFDESELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVYLMDCSF 240

Qy  249  DTISTSTVDTKLSFCDLFTHDEWINYDYLQSLKKYKGAGNPLGPTQGVGYNELIAR 308
Db  241  DTISTSTVDTKLSFCDLFTHDEWINYDYLQSLKKYKGAGNPLGPTQGVGYNELIAR 300

Qy  309  LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTV 368
Db  301  LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTV 360

Qy  369  ENITQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRVLRVNDRVVPLHGPCPVDALGRCTR 428
Db  361  ENITQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRVLRVNDRVVPLHGPCPVDALGRCTR 420

Qy  429  DSFVRGLSFARSGGDWAECEFA 449
Db  421  DSFVRGLSFARSGGDWAECEFA 441

RESULT 14
US-09-684-855-127
; Sequence 127, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 127
; LENGTH: 441
; TYPE: PRT
; ORGANISM: A. niger NRRL3135
; US-09-684-855-127

Query Match          98.4%; Score 2321; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.7e-231;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  9  NQSSCDTVDOGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARY 68
Db  1  NQSSCDTVDOGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARY 60

Qy  69  PTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSIGADDLTPFGQELVNSGKIFYOR 128
Db  61  PTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSIGADDLTPFGQELVNSGKIFYOR 120

Qy  129  YESLTRNIVPFISSGSSSRVIAAGKKEIEGFQSTKLKDPRAQPGQSSPKIDVVISEASS 188
Db  121  YESLTRNIVPFISSGSSSRVIAAGKKEIEGFQSTKLKDPRAQPGQSSPKIDVVISEASS 180

Qy  189  NNTLDPGCTCTVFDESELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVYLMDCSF 248
Db  181  NNTLDPGCTCTVFDESELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVYLMDCSF 240

Qy  249  DTISTSTVDTKLSFCDLFTHDEWINYDYLQSLKKYKGAGNPLGPTQGVGYNELIAR 308
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Qy  309  LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTV 368
Db  301  LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTV 360

Qy  369  ENITQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRVLRVNDRVVPLHGPCPVDALGRCTR 428
Db  361  ENITQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRVLRVNDRVVPLHGPCPVDALGRCTR 420

Qy  429  DSFVRGLSFARSGGDWAECEFA 449
Db  421  DSFVRGLSFARSGGDWAECEFA 441

RESULT 15
US-09-684-855-150
; Sequence 150, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 150
; LENGTH: 441
; TYPE: PRT
; ORGANISM: A. niger NRRL3135
; US-09-684-855-150

Query Match          98.4%; Score 2321; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.7e-231;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  9  NQSSCDTVDOGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARY 68
Db  1  NQSSCDTVDOGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARY 60

Qy  69  PTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSIGADDLTPFGQELVNSGKIFYOR 128
Db  61  PTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSIGADDLTPFGQELVNSGKIFYOR 120

Qy  129  YESLTRNIVPFISSGSSSRVIAAGKKEIEGFQSTKLKDPRAQPGQSSPKIDVVISEASS 188
Db  121  YESLTRNIVPFISSGSSSRVIAAGKKEIEGFQSTKLKDPRAQPGQSSPKIDVVISEASS 180

Qy  189  NNTLDPGCTCTVFDESELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVYLMDCSF 248
Db  181  NNTLDPGCTCTVFDESELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVYLMDCSF 240

Qy  249  DTISTSTVDTKLSFCDLFTHDEWINYDYLQSLKKYKGAGNPLGPTQGVGYNELIAR 308
Db  241  DTISTSTVDTKLSFCDLFTHDEWINYDYLQSLKKYKGAGNPLGPTQGVGYNELIAR 300
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Db	241	DTISTVTDTKLSPFCDLFTHDEWINVDYLOSLKKYYGHGAGNPLGPTQGVGYANELIAR	300
Qy	309	LTHSEVHDDTSSNHTLDSSPATEPLNSTLYADFSDNGIISILFALGLYNGTKPLSTTTV	368
Db	301	LTHSEVHDDTSSNHTLDSSPATEPLNSTLYADFSDNGIISILFALGLYNGTKPLSTTTV	360
Qy	369	ENITCTDGFSSAWTVFFASRLYVENMMQCAEQEPLVRVLVNDRVVPLHGCPCVDALGRCTR	428
Db	361	ENITCTDGFSSAWTVFFASRLYVENMMQCAEQEPLVRVLVNDRVVPLHGCPCVDALGRCTR	420
Qy	429	DSFVRGLSFARSGGDWAECPA	449
Db	421	DSFVRGLSFARSGGDWAECPA	441

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 24, 2004, 12:58:14 ; Search time 1060 Seconds
(without alignments)
137.139 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

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Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2353	99.8	467	14	US-10-229-358-5
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4	2350	99.7	467	16	US-10-662-914-22
5	2350	99.7	467	16	US-10-662-914-28
6	2349	99.6	467	16	US-10-662-914-8
7	2349	99.6	467	16	US-10-662-914-18
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18	2345	99.4	467	16	US-10-662-914-36
19	2345	99.4	467	16	US-10-662-914-42
20	2343	99.4	467	16	US-10-662-914-38
21	2343	99.4	467	16	US-10-662-914-69
22	2342	99.3	467	16	US-10-662-914-44
23	2341	99.3	467	13	US-10-083-452-11
24	2341	99.3	467	16	US-10-662-914-50
25	2341	99.3	467	16	US-10-662-914-52
26	2341	99.3	467	16	US-10-734-510-11
27	2340	99.2	467	16	US-10-662-914-54
28	2339	99.2	467	16	US-10-662-914-46
29	2339	99.2	467	16	US-10-662-914-48
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40	2277	96.6	441	14	US-10-442-538-103
41	2277	96.6	441	14	US-10-442-538-126
42	2277	96.6	441	14	US-10-442-538-148
43	2255	95.6	443	9	US-09-929-060-1
44	2242	95.1	443	9	US-09-929-060-2
45	1990	84.4	410	14	US-10-229-358-11

ALIGNMENTS

RESULT 1

US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie B. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-079-709-32

Query Match 99.8%; Score 2353; DB 14; Length 467;
Best Local Similarity 100.0%; Pred. No. 6.3e-208;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 79
QY 62 SRHGARYPTDSKGKYSALIEEIQONATTFDGKYAFKTYNYSIGADDLTPFGQEQLVNS 121
Db 80 SRHGARYPTDSKGKYSALIEEIQONATTFDGKYAFKTYNYSIGADDLTPFGQEQLVNS 139
QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVV 181
Db 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVV 199
QY 182 ISEASSNNLTDPGTCVTFEDELADTVEANFTATVPFSIRQRENDLSGVTLTDTEVTY 241
Db 200 ISEASSNNLTDPGTCVTFEDELADTVEANFTATVPFSIRQRENDLSGVTLTDTEVTY 259
QY 242 LMDMCSFDITISTVDTKLSPPCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGY 301
Db 260 LMDMCSFDITISTVDTKLSPPCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSSAWTVFFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPCVD 421
Db 380 PLSTTTVENITQTDGFSSAWTVFFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPCVD 439
QY 422 ALGCRTRDSFVRGLSFARSGDWAECFA 449
Db 440 ALGCRTRDSFVRGLSFARSGDWAECFA 467

RESULT 2
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian P.
; APPLICANT: Trinci, Anthony P.O.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger

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US-10-229-358-5

Query Match 99.8%; Score 2353; DB 14; Length 467;
Best Local Similarity 100.0%; Pred. No. 6.3e-208;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 79
QY 62 SRHGARYPTDSKGKYSALIEEIQONATTFDGKYAFKTYNYSIGADDLTPFGQEQLVNS 121
Db 80 SRHGARYPTDSKGKYSALIEEIQONATTFDGKYAFKTYNYSIGADDLTPFGQEQLVNS 139
QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVV 181
Db 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVV 199
QY 182 ISEASSNNLTDPGTCVTFEDELADTVEANFTATVPFSIRQRENDLSGVTLTDTEVTY 241
Db 200 ISEASSNNLTDPGTCVTFEDELADTVEANFTATVPFSIRQRENDLSGVTLTDTEVTY 259
QY 242 LMDMCSFDITISTVDTKLSPPCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGY 301
Db 260 LMDMCSFDITISTVDTKLSPPCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSSAWTVFFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPCVD 421
Db 380 PLSTTTVENITQTDGFSSAWTVFFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPCVD 439
QY 422 ALGCRTRDSFVRGLSFARSGDWAECFA 449
Db 440 ALGCRTRDSFVRGLSFARSGDWAECFA 467

RESULT 3
US-10-662-914-2
; Sequence 2, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mallaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-2

Query Match 99.8%; Score 2353; DB 16; Length 467;
Best Local Similarity 100.0%; Pred. No. 6.3e-208;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 79
QY 62 SRHGARYPTDSKGKYSALIEEIQONATTFDGKYAFKTYNYSIGADDLTPFGQEQLVNS 121
Db 80 SRHGARYPTDSKGKYSALIEEIQONATTFDGKYAFKTYNYSIGADDLTPFGQEQLVNS 139

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122 GIKFYQYESLTRNIVPIRSGSSRVIASGKKEIEGQSTKLDKDPRAQPGSSPKIDVV 181
Db
140 GIKFYQYESLTRNIVPIRSGSSRVIASGKKEIEGQSTKLDKDPRAQPGSSPKIDVV 199
Qy 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTY 241
Db 200 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTY 259
Qy 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINDYLSLKKYGHGAGNPLGPTQGVY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINDYLSLKKYGHGAGNPLGPTQGVY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 4
US-10-662-914-22
; Sequence 22, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-22

Query Match 99.7%; Score 2350; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.2e-207;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPACGRVTFAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPACGRVTFAQVL 79
Qy 62 SRHGARYPTDSKGKYSALIEIEIQONATTFDGKYAFKTYNYSIGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGKYSALIEIEIQONATTFDGKYAFKTYNYSIGADDLTPFGQELVNS 139
Qy 122 GIKFYQYESLTRNIVPIRSGSSRVIASGKKEIEGQSTKLDKDPRAQPGSSPKIDVV 181
Db 140 GIKFYQYESLTRNIVPIRSGSSRVIASGKKEIEGQSTKLDKDPRAQPGSSPKIDVV 199
Qy 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTY 241
Db 200 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTY 259
Qy 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINDYLSLKKYGHGAGNPLGPTQGVY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINDYLSLKKYGHGAGNPLGPTQGVY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 5
US-10-662-914-28
; Sequence 28, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 28
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-28

Query Match 99.7%; Score 2350; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.2e-207;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPACGRVTFAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPACGRVTFAQVL 79
Qy 62 SRHGARYPTDSKGKYSALIEIEIQONATTFDGKYAFKTYNYSIGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGKYSALIEIEIQONATTFDGKYAFKTYNYSIGADDLTPFGQELVNS 139
Qy 122 GIKFYQYESLTRNIVPIRSGSSRVIASGKKEIEGQSTKLDKDPRAQPGSSPKIDVV 181
Db 140 GIKFYQYESLTRNIVPIRSGSSRVIASGKKEIEGQSTKLDKDPRAQPGSSPKIDVV 199
Qy 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTY 241
Db 200 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTY 259
Qy 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINDYLSLKKYGHGAGNPLGPTQGVY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINDYLSLKKYGHGAGNPLGPTQGVY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 6
US-10-662-914-8
; Sequence 8, Application US/10662914


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Db 80 SRHGARYPTDSKGYKYSALIEIEIQNATTFDGYAF.LKTYNSLGADDLTPFGQELVNS 139
Qy 122 GIKFYQRYESLTRNIVPPIRSSGSSRVASGKKIEGQSTKLDPPRAQPGQSSPKIDV 181
Db 140 GIKFYQRYESLTRNIVPPIRSSGSSRVASGKKIEGQSTKLDPPRAQPGQSSPKIDV 199
Qy 182 ISEASSNNLTDPGCTCTVFEDSELADTVANFTATFVPSIRQLENDLSGVTLDTEVTY 241
Db 200 ISEASSNNLTDPGCTCTVFEDSELADTVANFTATFVPSIRQLENDLSGVTLDTEVTY 259
Qy 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLSDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 9
US-10-662-914-24
; Sequence 24, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 24
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-24
Query Match 99.6%; Score 2349; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.5e-207;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 79
Qy 62 SRHGARYPTDSKGYKYSALIEIEIQNATTFDGYAF.LKTYNSLGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGYKYSALIEIEIQNATTFDGYAF.LKTYNSLGADDLTPFGQELVNS 139
Qy 122 GIKFYQRYESLTRNIVPPIRSSGSSRVASGKKIEGQSTKLDPPRAQPGQSSPKIDV 181
Db 140 GIKFYQRYESLTRNIVPPIRSSGSSRVASGKKIEGQSTKLDPPRAQPGQSSPKIDV 199
Qy 182 ISEASSNNLTDPGCTCTVFEDSELADTVANFTATFVPSIRQLENDLSGVTLDTEVTY 241
Db 200 ISEASSNNLTDPGCTCTVFEDSELADTVANFTATFVPSIRQLENDLSGVTLDTEVTY 259
Qy 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLSDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467
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Qy 302 ANELIARLTHSPVHDDTSSNHTLSDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 10
US-10-662-914-34
; Sequence 34, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 34
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-34
Query Match 99.6%; Score 2349; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.5e-207;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 79
Qy 62 SRHGARYPTDSKGYKYSALIEIEIQNATTFDGYAF.LKTYNSLGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGYKYSALIEIEIQNATTFDGYAF.LKTYNSLGADDLTPFGQELVNS 139
Qy 122 GIKFYQRYESLTRNIVPPIRSSGSSRVASGKKIEGQSTKLDPPRAQPGQSSPKIDV 181
Db 140 GIKFYQRYESLTRNIVPPIRSSGSSRVASGKKIEGQSTKLDPPRAQPGQSSPKIDV 199
Qy 182 ISEASSNNLTDPGCTCTVFEDSELADTVANFTATFVPSIRQLENDLSGVTLDTEVTY 241
Db 200 ISEASSNNLTDPGCTCTVFEDSELADTVANFTATFVPSIRQLENDLSGVTLDTEVTY 259
Qy 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLSDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467
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Db 20 LAVPASRNQSSCDTVDQGYQCFSFETSHLWGYAPFFSLANESVISPEVPAGCRVTFAQVL 79
Qy 62 SRHGARYPTDSKGGKYSALIEIQONATTFDQKYAFKTYNYSIGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGGKYSALIEIQONATTFDQKYAFKTYNYSIGADDLTPFGQELVNS 139
Qy 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKDPRAQPGQSSPKIDVW 181
Db 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKDPRAQPGQSSPKIDVW 199
Qy 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTEVTY 241
Db 200 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTEVTY 259
Qy 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINVDYLSQSLKYYGHGAGNPLGPTQGVGY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINVDYLSQSLKYYGHGAGNPLGPTQGVGY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDFSSAWTVPFASRLYVEMMOCQAEQEBPLVRVLVNDRVVPLHGCPCVD 421
Db 380 PLSTTTVENITQTDFSSAWTVPFASRLYVEMMOCQAEQEBPLVRVLVNDRVVPLHGCPCVD 439
Qy 422 ALGRCTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGRCTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 14

US-10-662-914-32
; Sequence 32, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H. J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES

; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-32

Query Match 99.5%; Score 2347; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.3e-207;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LAVPASRNQSSCDTVDQGYQCFSFETSHLWGYAPFFSLANESVISPEVPAGCRVTFAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSFETSHLWGYAPFFSLANESVISPEVPAGCRVTFAQVL 79
Qy 62 SRHGARYPTDSKGGKYSALIEIQONATTFDQKYAFKTYNYSIGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGGKYSALIEIQONATTFDQKYAFKTYNYSIGADDLTPFGQELVNS 139
Qy 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKDPRAQPGQSSPKIDVW 181
Db 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKDPRAQPGQSSPKIDVW 199
Qy 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTEVTY 241
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Qy 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINVDYLSQSLKYYGHGAGNPLGPTQGVGY 301
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Qy 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 361
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RESULT 15

US-10-662-914-12
; Sequence 12, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H. J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES

; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-12

Query Match 99.5%; Score 2346; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.8e-207;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LAVPASRNQSSCDTVDQGYQCFSFETSHLWGYAPFFSLANESVISPEVPAGCRVTFAQVL 61
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Qy 62 SRHGARYPTDSKGGKYSALIEIQONATTFDQKYAFKTYNYSIGADDLTPFGQELVNS 121
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Qy 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKDPRAQPGQSSPKIDVW 181
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Qy 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINVDYLSQSLKYYGHGAGNPLGPTQGVGY 301
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Qy 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDFSSAWTVPFASRLYVEMMOCQAEQEBPLVRVLVNDRVVPLHGCPCVD 421
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Qy 422 ALGRCTRDSFVRGLSFARSGGDWAECEFA 449

Db 440 ALGRCTRDSEVRGLSFARSGDWAECEFA 467

Search completed: October 24, 2004, 13:24:29
Job time : 1062 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 13:00:14 ; Search time 7951 Seconds
(without alignments)
2670.491 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2358	100.0	1350	12	AF295325
2	2353	99.8	1404	6	AI9452
3	2353	99.8	1404	6	I13430
4	2353	99.8	1404	6	I33881

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RESULT 1
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LOCUS     SYNTHETIC construct phytase mRNA, complete cds.
DEFINITION
ACCESSION AF295325
VERSION    AF295325.1
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 1350)
AUTHORS    Yang,L., Chen,Z., Bei,J., Liao,L. and Wang,X.
TITLE      Synthetic sequence of phytase gene for expression in Pichia
           pastoris
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 1350)
AUTHORS    Chen,Z.
TITLE      Direct Submission
JOURNAL    Submitted (11-AUG-2000) Animal Science Institute, Guangdong Academy
           of Agricultural Sciences, Guangzhou, Guangdong 510640, China
REFERENCE  3 (bases 1 to 1350)
AUTHORS    Yang,L., Bei,J., Liao,L. and Wang,X.
TITLE      Direct Submission
JOURNAL    Submitted (11-AUG-2000) Biopharmaceutical Center, Zhongshan
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ORIGIN

Alignment Scores:

Pred. No.:	2,55e-187	Length:	1350
Score:	2358.00	Matches:	449
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-089-364-4 (1-449) x AF295325 (1-1350)

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QY	21	GlnCysPheSerGluThrSerHisLeuTrpGlnTyrAlaProPheSerLeuAla	40
Db	61	CAATGTTCTCCGAGACTTCTCATCTTTGGGGTCAATACGACCACTTCTCTCTGGCA	120
QY	41	AsnGluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnVal	60
Db	121	AACGAATCTGTCATCTCCCTGAGGTGCCAGCGGAGTAGAGTACATTTTCGCTCAGGTC	180
QY	61	LeuSerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeu	80
Db	181	CTTTCAGACATCGAGCTAGATATCCACCGACTCCCAAGGGTAAGAAATATCCGGCTCTT	240
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Db	241	ATTGAGGAGATCCAGAGAAGCGTACCACCTTTGACGGAAATATGCTTCTCTGAAGACA	300
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Db	301	TACAACCTACTCTTTGGGTGAGATGACCTCACTCCATTCGGAGAACAGGAGCTGTCAAC	360
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QY	161	SerThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspVal	180
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QY	201	GluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSer	220
Db	601	GAGAGACTCTGAATTTGGCCGTAAGTGTGCGAAGCCAAATTTCACTGCGCACTTTTCGTCCCATCC	660

QY	221	IleArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThr	240
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QY	241	TyrLeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeu	260
Db	721	TACCTTATGGACATGTGTTCCCTTCGACACTATCTCCACTTCTACCGTCGACACCAAGCTG	780
QY	261	SerProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspThrLeuGlnSer	280
Db	781	TCCCCAATCTGTGACTGTTTCCATCCCATGACGAATGGATCAACTTACGACTCTTGAGTCC	840
QY	281	LeuLysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGly	300
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QY	301	TyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSer	320
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QY	321	AsnHisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAsp	340
Db	961	AACCAACATTTGGACTCTTCTCCAGCTACCTTTCATTTGCACTTACTTACTTGTACGCTGAC	1020
QY	341	PheSerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThr	360
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QY	361	LysProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAla	380
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QY	421	AspAlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSer	440
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QY	441	GlyGlyAspTrpAlaGluCysPheAla	449
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RESULT 2

LOCUS A19452

DEFINITION phytase cDNA fragment.

ACCESSION A19452

VERSION A19452.1

GI:583195

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 1404)

AUTHORS van Gorcom,R.F.M., van Hartingsveldt,W., van Paridon,P.A., Veenstra,A.E., IJtten,R.G.M. and Seiten,G.C.M.

TITLE Cloning and expression of microbial phytase

JOURNAL Patent: EP 0420358-A 41 03-APR-1991;

FEATURES

Location/Qualifiers

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ORIGIN

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Alignment Scores:
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 6 Gaps: 0

US-10-089-364-4 (1-449) x A19452 (1-1404)

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Db 118 TGCCTTCCGAGACTTCGATCTTTGGGGTCAATACCGCACCGTCTTCTCTCTGGCAAA 177
Qy 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 178 GAATCGGTCATCTCCCTCGAGTGCCCGCGATGACAGTACATCTTCGTCAGGTCCTC 237
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RESULT 3
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REFERENCE 1 (bases 1 to 1404)
AUTHORS Van Gorm, R.F.M., Van Hartingsveldt, W., Van Paridon, P.A.,
Veenstra, A.E., Luiten, R.G.M. and Selden, G.C.M.
TITLE Cloning and expression of phytase from aspergillus
JOURNAL Patent: US 5436156-A 33 25-JUL-1995;
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Location/Qualifiers
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VERSION AR195149.1 GI:20244586
KEYWORDS
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ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1404)
AUTHORS Van Gorcom,R.F.M., Van Hartingsveldt,W., Van Paridon,P.Andreas.,
Veenstra,A.Eveline., Luiten,R.G.M. and Sellen,G.C.M.
TITLE Cloning and expression of phytase from aspergillus
JOURNAL Patent: US 6350602-A 33 26-FEB-2002;
FEATURES Location/Qualifiers
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REFERENCE 1 (bases 1 to 2000)
AUTHORS van Hartingsveldt, W., Van Zeijl, C.M.J., Harteveld, M.G., Gouka, R.J.,
Suykerbyk, M.E.G., Luiten, R.G.M., Van Paridon, P.A., Selden, G.C.M.,
Veenstra, A.E., Van Gorcom, R.F.M. and Van Den Hondel, C.A.M.J.
Cloning, molecular characterization and overexpression of the
phyA gene (phyA) of Aspergillus niger
JOURNAL Gene (1992) In press
AUTHORS van Hartingsveldt, W.
TITLE Direct Submission
JOURNAL Submitted (05-OCT-1992) Van Hartingsveldt W., TNO Medical
Biological Laboratory, Lange Kleiweg 139, Rijswijk, the Netherlands
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 VERSION M94550
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 REFERENCE 1 (bases 1 to 2665)
 AUTHORS Mullane, E.J., Gibson, D.M. and Ullah, A.H.
 TITLE Positive identification of a lambda gt11 clone containing a region of fungal phytase gene by immunoprobe and sequence verification
 JOURNAL Appl. Microbiol. Biotechnol. 35 (5), 611-614 (1991)
 MEDLINE 92000601
 PUBMED 1369340
 REFERENCE 2 (bases 1 to 2665)
 AUTHORS Mullane, E.J.
 TITLE Sequence of the Aspergillus niger (ficum) phytase gene
 JOURNAL Unpublished (1992)
 COMMENT Original source text: Aspergillus niger (library: EMBL 3; NRRL 3135) DNA.
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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
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ACCESSION A19451
VERSION A19451.1 GI:583193
KEYWORDS synthetic construct
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ORGANISM
REFERENCE 1 (bases 1 to 6756)
AUTHORS van Gorcom,R.F.M., van Hartingsveldt,W., van Paridon,P.A.,
Veenstra,A.E., Luiten,R.G.M. and Seltlen,G.C.M.
TITLE Cloning and expression of microbial phytase
JOURNAL Patent: EP 0420358-A 40 03-APR-1991;
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AUTHORS Van Gorcom,R.F.M., Van Hartingsveldt,W., Van Paridon,P.A.,
Veenstra,A.E., Luiten,R.G.M. and Seiten,G.C.M.
TITLE Cloning and expression of phytase from aspergillus
JOURNAL Patent: US 5436156-A 31 25-JUL-1995;
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AUTHORS Van Gormom,R.F.M., Van Hartingsveldt,W., Van Paridon,P.Andreas.,
Veenstra,A.Eveline., Iuiten,R.G.M. and Seiten,G.C.M.
TITLE Cloning and expression of phytase from aspergillus
JOURNAL Patent: US 6350602-A 31 26-FEB-2002;
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Peng, Y.Y., Zhou, Z.Y. and Ma, L.P.
Cloning and characterization of phytase gene of Aspergillus niger
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Unpublished
2 (bases 1 to 1525)
REFERENCE Peng, Y.Y., Zhou, Z.Y. and Ma, L.P.
AUTHORS Direct Submission
TITLE Submitted (01-OCT-2003) College of Animal Science & Technology,
JOURNAL Southwest Agricultural University, Tiansheng, Beibei, Chongqing
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 Turunen,M.K. and Fagerstrom,R.B.
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 Miettinen-Oinonen,A.S.K., Turunen,M.K., Rambossek,J.A.,
 Piddington,C.S., Houston,C.S. and Cantrell,M.A.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	2353	99.8 1404 1	US-08-151-574-33
2	2353	99.8 1404 1	Sequence 33, Appl
3	2353	99.8 1404 1	Sequence 19, Appl
4	2353	99.8 1404 1	Sequence 1, Appl
5	2353	99.8 1404 1	Sequence 33, Appl
6	2353	99.8 1404 3	Sequence 33, Appl
7	2353	99.8 6756 2	US-08-151-574-31
8	2353	99.8 6756 2	Sequence 31, Appl
9	2309	97.9 2363 1	US-07-923-724-7
10	2309	97.9 2363 2	Sequence 7, Appl
11	2309	97.9 2379 2	Sequence 1, Appl
12	2278	96.6 1515 3	US-09-155-855-5

13	2278	96.6	1515	3	US-09-543-744-5	Sequence 5, Appl
14	2278	96.6	1515	4	US-09-929-060-5	Sequence 5, Appl
15	2255	95.6	1332	3	US-09-155-855-4	Sequence 4, Appl
16	2255	95.6	1332	3	US-09-543-744-4	Sequence 4, Appl
17	2255	95.6	1332	4	US-09-929-060-4	Sequence 4, Appl
18	1929	81.8	1426	4	US-09-684-855-168	Sequence 168, App
19	1929	81.8	1426	4	US-09-488-265B-34	Sequence 34, Appl
20	1833	77.7	1404	4	US-09-684-855-162	Sequence 162, App
21	1833	77.7	1404	4	US-09-488-265B-28	Sequence 28, Appl
22	1828	77.5	1404	4	US-09-488-265B-92	Sequence 92, Appl
23	1828	77.3	1404	4	US-09-488-265B-92	Sequence 92, Appl
24	1820	77.2	1426	4	US-09-684-855-140	Sequence 140, App
25	1820	77.2	1426	4	US-09-488-265B-25	Sequence 25, Appl
26	1818	77.1	1426	3	US-09-121-425-3	Sequence 3, Appl
27	1818	77.1	1426	4	US-09-634-493A-3	Sequence 3, Appl
28	1818	77.1	1426	4	US-09-684-855-117	Sequence 117, App
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31	1806	76.6	1404	4	US-09-684-855-164	Sequence 164, App
32	1806	76.6	1404	4	US-09-488-265B-30	Sequence 30, Appl
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34	1770	75.1	1912	3	US-08-868-435-11	Sequence 11, Appl
35	1770	75.1	1912	4	US-08-744-231-11	Sequence 11, Appl
36	1617.5	68.6	1571	3	US-09-635-504-11	Sequence 11, Appl
37	1617.5	68.6	1571	3	US-08-868-435-32	Sequence 32, Appl
38	1617.5	68.6	1571	3	US-08-744-231-32	Sequence 32, Appl
39	1617.5	68.6	1571	3	US-09-044-718-10	Sequence 10, Appl
40	1617.5	68.6	1571	4	US-09-635-504-32	Sequence 32, Appl
41	1617.5	68.6	1571	4	US-10-062-848-10	Sequence 10, Appl
42	1610.5	68.3	1404	4	US-09-684-855-166	Sequence 166, App
43	1610.5	68.3	1404	4	US-09-488-265B-32	Sequence 32, Appl
44	1534	65.1	1931	3	US-08-868-435-28	Sequence 28, Appl
45	1534	65.1	1931	3	US-08-744-231-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-151-574-33
; Sequence 33, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Seltien
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151.574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688, 578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.

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; REGISTRATION NUMBER: 29, 959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficum (Aspergillus niger)
; STRAIN: NRRL 3135
; US-08-151-574-33

Alignment Scores:
Pred. No.: 1,31e-275 Length: 1404
Score: 2353.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 1 Gaps: 0

US-10-089-364-4 (1-449) x US-08-151-574-33 (1-1404)

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DB 238 TCCCGTCATGAGCGGGTATCCGACCGACTCCAAAGGGCAAGAAATACTCCGCTCAT 297
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DB 298 GAGGAGATCCAGCAGACGCGACCCACTTTGACGGAAATATGCTTCTCCCTGAAGACATAC 357
QY 102 AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
DB 358 AACTACAGCTTGGTGCAGATGACCTGACTCCCTTCGGAGACAGGAGTAGTCAACTCC 417
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerIleuThrArgAsnIleValProPheIleArg 141
DB 418 GGCATCAAGTCTTACCAGCGGTACGATCGCTCAAGGAACATCGTTCCTCATTCATCCGA 477
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlySer 161
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QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
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DB 1198 ACGTTTCGGTTTGGTTCGCTGAGTGTAGTGTGATGATGATGATGATGATGATGATGAT 1257
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
DB 1258 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
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RESULT 2
US-08-146-424-19
; Sequence 19, Application US/08146424
; Patent No. 5593963
; GENERAL INFORMATION:
; APPLICANT: VAN OOLJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRION
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/146,424
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/DOCKET NUMBER: 44615-20011.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
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; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 70
; US-08-146-424-19
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; Alignment Scores:
; Pred. No.: 1,31e-275 Length: 1404
; Score: 2353.00 Matches: 448
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 99.79% Indels: 0
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; QY 182 IleSerGluAlaSerSerSerAsnThrLeuAspProGlyThrCysThrValPheGlu 201
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; QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
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; QY 222 ArgGlnArgLeuGluAlaAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
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; QY 262 ProPheCysAspLeuPheThrHisAspGluTyrIleAsnTyrAspTyrIleuGlnSerLeu 281
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; QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
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; QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
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; QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
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; QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
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; QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
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; QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
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; QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
; DB 1258 CCGCTGTGCTGCTTGTGTTAATGATCGCGTTGTCGCGTGCATGGGTGTCGGTTGAT 1317
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; QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
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; QY 442 GlyAspTrpAlaGluCysPheAla 449
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;
; RESULT 3
; US-08-693-709-1
; Sequence 1, Application US/08693709
; Patent No. 5770413
; GENERAL INFORMATION:
; APPLICANT: VAN OIJEN, ALBERT J.J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN JAN
; APPLICANT: SIMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA

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COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/693,709
 FILING DATE: 07-AUG-1996
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/146,424
 FILING DATE: 02-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 24615-20011.10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-813-5600
 TELEFAX: 415-494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1404 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 1..1401
 OTHER INFORMATION:
 NAME/KEY: mat_peptide
 LOCATION: 70..1401
 OTHER INFORMATION:
 NAME/KEY: Signal Sequence
 LOCATION: 1..72
 OTHER INFORMATION:
 US-08-693-709-1

Alignment Scores:
 Pred. No.: 1,31e-275 Length: 1404
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 1 Gaps: 0

US-10-089-364-4 (1-449) x US-08-693-709-1 (1-1404)

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 DB 58 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGGCATCGGTGCAATCGGGGTATCAA 117
 QY 22 CysPheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsn 41
 DB 118 TGTCTTCCGAGACTTGGCATCTTTGGGTCAATACGACCGTCTCTCTCGCAAC 177
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 DB 178 GAATCGGTCACTCCCTGAGGTCCCGCCGGATGCAAGTCACTTTCCGTCCAGTCTC 237
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
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 DB 298 GAGGAGATCCAGCAGACGCGACCCACTTTCACGGAAATATGCCCTTCTCGAGACATAC 357
 QY 102 AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 DB 358 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGAGAACAGAGGCTAGTCAACTCC 417

QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 DB 418 GGCATCAAGTTCTACGAGGGTACGAATCGCTCAACAGGAACATCGTTCCATTCAATCCGA 477
 QY 142 SerSerGlySerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 DB 478 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATGAGGGCTTCAGAGAC 537
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
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 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
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 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
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 DB 1138 CCGCTATCTACACGACCGGTGGAGAAATATCACCGACAGATGGAATCTCGTCTGTCTGG 1197
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 DB 1198 ACGGTTCCGTTTGTCTTCGCGTTGTACGTGAGATGATGAGTGTAGGCGAGACAGAG 1257
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 DB 1258 CCGCTGTCTCGTGTCTTGGTTATGATCGGTTGTCCCGCTGCACTGGGTGTCCGTTGAT 1317
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 DB 1318 GCTTTGGGGAGATGATCCCGGATAGCTTTGTGAGGGGGTGTGAGCTTTGTAGATCTGGG 1377
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 DB 1378 GGTGATTGGCGGAGTGTCTTGTCT 1401

RESULT 4

US-08-419-448-33

; Sequence 33, Application US/08419448

; Patent No. 5863533

; GENERAL INFORMATION:
 ; APPLICANT: Robert F.M. Van Gorcom
 ; APPLICANT: Willem Van Hartingsveldt
 ; APPLICANT: Petrus A. Van Paridon
 ; APPLICANT: Annemarie E. Veenstra
 ; APPLICANT: Rudolf G.M. Luttin
 ; APPLICANT: Gerardus Selden
 ; TITLE OF INVENTION: Cloning and Expression of Microbial
 ; TITLE OF INVENTION: Phytase
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Mortison & Foerster
 ; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 ; CITY: Washington
 ; STATE: D. C.
 ; COUNTRY: USA
 ; ZIP: 20006-1888
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/419,448
 ; FILING DATE: 10-APR-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murashige, Kate H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 24615-20026.10
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-887-1500
 ; INFORMATION FOR SEQ ID NO: 33:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1404 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Aspergillus ficuum (Aspergillus niger)
 ; STRAIN: NRRL 3135
 ; US-08-419-448-33

Alignment Scores:
 Pred. No.: 1,31e-275 Length: 1404
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 2 Gaps: 0

US-10-089-364-4 (1-449) x US-08-419-448-33 (1-1404)

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 Qy 22 CysPheSerGluThrSerHisLeuTyrGlnTyrAlaProPheSerLeuAlaAsn 41
 Db 118 TGCCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGCTTCTCTCGCAAC 177
 Qy 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 178 GAATCGGTCACTCTCCCTGAGTGGCCCGGATGCGAGTCACTTTGCTCAGGTCTC 237
 Qy 62 SerArgHisGlyValArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeu 81
 Db 238 TCCGTCATGGAGCGCGGTATCCGACCGACTCCAAAGGCGCAAGAAATACTCCGCTCTCAT 297

Qy 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 298 GAGGAGATCCAGCAGAACCGGACCACCTTTGACGGAAATATATCCCTTCTCGAAGACATAC 357
 Qy 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 358 AACTACAGCTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGGAGTAGTCACTCC 417
 Qy 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 418 GGCATCAAGTTCTTACGAGCGGTACGAATCGCTCACAAAGGAACATCGTTCATTCATCCGA 477
 Qy 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 478 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCAGGGCTTCCAGAGC 537
 Qy 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 538 ACCAAGCTGAAGGATCCTCGTCCAGCCCGGCCAATCGTCGCCCAAGATCGACGTGGTC 597
 Qy 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
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 Db 658 GACAGCGAATTGGCCGATACCGTCCGAAGCCAAATTCACGCCACCGTTCGTCCCTCCATT 717
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 Db 718 CGTCAACGCTCTGGAGAACGACCTGTCGGTGTGACTCTCACAGACACAGAAAGTGACCTAC 777
 Qy 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 778 CTCATGGACATGTGCTCTCTCGACACCATCTCCACACGACCGCTCGACACCAAGCTGCC 837
 Qy 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 838 CCCTTCTGTGACCTGTTCCACCATGACGAATGGATCAACTAGACTACTCCAGTCCCTTG 897
 Qy 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 898 AAAAAATATTACGGCCATGTGTCAGGTAAACCGCTCGGCCCGACCCAGGGGTGCGCTAC 957
 Qy 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 958 GCTAACGAGCTCATCGCCCGCTCTGCCACTCGCTCTGTCCAAGATGACACCAAGTCCAAC 1017
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 Db 1018 CACACTTGGACTCGAGCCCGGCTACCTTCCGCTCAACTCTACTCTCTACCGCGGACTTT 1077
 Qy 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1078 TCGCATGACAAACGGCATCATCTCCATTCTCTTCTTTAGTCTGTACACAGGCACTAAG 1137
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 Db 1138 CCGCTATCTACACAGCCGCTGGAGAATATCACCCAGACAGATGGATTCCTCTCTGCTTGG 1197
 Qy 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1198 ACGGTTCCGTTTGTCTTCGCTTTGTACGTGAGATGATGAGTGTGAGGCGGAGCAGAG 1257
 Qy 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 1258 CCGTGTGTCGTCTTGGTTAATGATCGGCTTGTCCGCTGCATGGGTGCTCCGGTGTAT 1317
 Qy 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1318 GCTTTGGGGAGATGTATCCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGTAGATCTGGG 1377
 Qy 442 GlyAspTrpAlaGluCysPheAla 449

Db 1198 ACGGTTCCGTTTGGCTTTCGGCTTTGACGTGCGAGATGATGACGTGTCAGCGGAGCAGGAG 1257
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QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
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RESULT 6

US-08-151-574-31
; Sequence 31, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
; IMMEDIATE SOURCE:
; LIBRARY: lambda AF
; CLONE: pAF2-3, pAF2-6, pAF2-7
; FEATURE:
; NAME/KEY: exon
; LOCATION: 210..253
; FEATURE:

; NAME/KEY: intron
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; LOCATION: join(210..253, 356..1715)
; OTHER INFORMATION: /codon_start= 210
; OTHER INFORMATION: /product= "Phytase"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 210..380
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; OTHER INFORMATION: /product= "Phytase"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; US-08-151-574-31
Alignment Scores:
Pred. No.: 1.95e-274 Length: 6756
Score: 2353.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 1 Gaps: 0
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QY 22 CysPheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPheSerLeuAlaAsn 41
Db 429 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGTTCTTCTCTCGCAAC 488
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 489 GAATCGGTCACTCTCCCTGAGGTCCCGCGGATGAGATCACTTTCGCTCAGTCTC 548
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerHisGlyLysLysTyrSerAlaLeuIle 81
Db 549 TCCCGTCATGGAGCGGTATCCGACCGACTCCAAAGGCAAGAAATACTCGCTCTCAT 608
QY 82 GluGluIleGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 609 GAGGATCCAGCAGAACGCGACCCACTTTGACGGAATAATATGCTTCTCGAAGACATAC 668
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db 669 AACTACAGCTTGGTGAGATGACCTGACCTTCCTTCGAGAAATAATATGCTTCTCGAAGACATAC 728
QY 122 GlyTleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 729 GGCATCAAGTTCTACCAAGCGGTACGAATCGCTCACAAGGAACATCGTTCCTTCCATCCGA 788
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db 789 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGGAAGAAATTCATCGAGGGGTTCCAGAGC 848
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 849 ACCAAGCTGAGGATCTCTGTCGCCAGCCCGCCCAATCGTCCGCCAAGATCGAGCTGGTC 908
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db 909 ATTTCCGAGGCCAGCTCATCCCAACAACACTCTCGACCCAGGCACCTGCACTGCTTCGAA 968

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QY	222	ArgGluArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr	241
DB	1029	CGTCAACGCTCTGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAAGTGACCTAC	1088
QY	242	LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer	261
DB	1089	CTCATGAGCATGTGCTCTTCGACACCATCTCCACGACACCGTCGACACCAAGCTGCC	1148
QY	262	ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTrpAspTyrLeuGlnSerLeu	281
DB	1149	CCCTTCGTGACCTGTTTACCCATGACGAATGGATCAACTTACGACTACCTTCCAGTCCCTTG	1208
QY	282	LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr	301
DB	1209	AAAAGATATTACGGCCATGTGTGAGGTAAACCCGCTCGGCCCGACCCAGGCGTCGGCTAC	1268
QY	302	AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn	321
DB	1269	GCTAACAGAGTCTATCGCCGCTGACCCCATCGCTCTCCAGATGACACCACTTCCAAC	1328
QY	322	HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe	341
DB	1329	CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTACGGCGGACTTT	1388
QY	342	SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys	361
DB	1389	TCGCATGACACGGCATCATCTCCATTCTCTTTAGTCTGTGTACAACGGCAGCTAAG	1448
QY	362	ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp	381
DB	1449	CCGTATCTACACGACCGTGGAGAAATACCCACAGACAGATGAATCTCGTCTGCTTGG	1508
QY	382	ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu	401
DB	1509	ACGGTTCCGTTTGCTTCGCTTTGTACGTCAGATGATGACAGTCTCAGGCGGAGCAGAG	1568
QY	402	ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp	421
DB	1569	CCGCTGGTCCGTGTCTTGTTAAATGATCCGCTTGTCCCGCTGATGGGTGTCGGTTGAT	1628
QY	422	AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly	441
DB	1629	GCTTTGGGGAGATGTACCCGGATAGCTTTGTAGGGGGTTGAGCTTTGCTAGATCTGGG	1688
QY	442	GlyAspTrpAlaGluCysPheAla	449
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RESULT 7

AB001.
 US-08-419-448-31
 ? Sequence 31, Application US/08419448
 ? Patent No. 5863533
 ?
 ? GENERAL INFORMATION:
 ? APPLICANT: Robert F.M. Van Gorcum
 ? APPLICANT: Willem Van Hartingsveldt
 ? APPLICANT: Petrus A. Van Paridon
 ? APPLICANT: Annemarie E. Veenstra
 ? APPLICANT: Rudolf G.M. Luttin
 ? APPLICANT: Gerardus Seltien
 ? TITLE OF INVENTION: Cloning and Expression of Microbial
 ? TITLE OF INVENTION: Phytase
 ? NUMBER OF SEQUENCES: 52
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Morrison & Foerster
 ? STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 ? CITY: Washington
 ? STATE: D.C.
 ? COUNTRY: USA
 ? ZIP: 20006-1888
 ?
 ? OTHER INFORMATION: phosphate= "Phytase"
 ; OTHER INFORMATION: /product= "Phytase"
 ; OTHER INFORMATION: /evidence= EXPERIMENTAL
 ;
 US-08-419-448-31
 Alignment Scores:
 Pred. No.: 1,95e-274 Length: 6756
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 2 Gaps: 0
 US-10-089-364-4 (1-449) x US-08-419-448-31 (1-6756)
 QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValaspGlnGlyTyrGln 21
 Db 369 CTGCACGTCCCGCCCTCGAGAAATCAATCCAGTTGGATACGGTCGATCAGGGGTATCAA 428
 QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41

Db 429 TGCTTCTCCGAGACTTCGATCTTTGGGGTCAATACGACCGCTTCTTCTCTCTGCAAAAC 488
Qy 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGluValIleu 61
Db 489 GAATCGGTCATCTCCCTCGAGTGCCCGCGGATGCAGAGTCACTTTTCGCTCAGGTCCTC 548
Qy 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
Db 549 TCCCGTCATGAGCGCGGTATCCGACCGACTCCAGGGCCAGAAATATGCTTCTCTGAAGACATAC 608
Qy 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 609 GAGGAGATCCAGCAGAACCGCACCACTTTGACGGAATAATATGCTTCTCTGAAGACATAC 668
Qy 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db 669 AACTACAGCTTGGGTGGAGATGACTGACTCCCTTCGGAGAACAGGACTAGTCAACTCC 728
Qy 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 729 GGCAATCAAGTTCTACCAAGCGGTACGATCGCTCACAGGAACATCGTTCCATTCATCCGA 788
Qy 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
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Qy 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 849 ACCAAGCTGAAGGATCCTCGTGGCCAGCCCGCCCAATCGTCCGCAAGATCGAGTGGTC 908
Qy 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
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Db 1269 GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCTGTCCAGATGACACAGTCCAC 1328
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Db 1389 TCGATGACACAGCGGATCATCTCCATTCTCTTGTCTTAGTCTGTACACGCGCACTAAG 1448
Qy 362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db 1449 CCGTATCTACACAGCGGTGGAGATATATCCACAGATGATGATTCCTGCTGCTGG 1508
Qy 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401

Db 1509 ACGGTCCGTTTGTCTCCGTTTGTAGCTCGAGATGATGACGTGTACGCGGAGCAGGAG 1568
Qy 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
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RESULT 8
US-09-233-510-31
; Sequence 31, Application US/09233510
; Patent No. 6350602
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,510
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
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; LIBRARY: lambda AF
; CLONE: pAF2-3, pAF2-6, pAF2-7
; FEATURE:
; NAME/KEY: exon
; LOCATION: 210..253

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Qy	222	ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr	241
Db	1029	CGTCAACGCTCGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAAGTGACCTAC	1088
Qy	242	LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer	261
Db	1089	CTCATGACATGTGCTCTTCGACACCAATCTCACAGACCGCTGACACCAAGCTGTCC	1148
Qy	262	ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu	281
Db	1149	CCCTTCGTGACCTGTTACCCATGACGATGGATCAACTACGACCTACCTCCAGTCCTTG	1208
Qy	282	LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr	301
Db	1209	AAAAAGTATTACGGCCATGGTGCAGGTAAACCCGCTCGCGCCGACCCAGGGCGTTCGGGTAC	1268
Qy	302	AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn	321
Db	1269	GCTAACAGAGCTCATGCCCGCTGACCCCATCGGCTGTCCACGATGACACCGATTCCCAAC	1328
Qy	322	HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe	341
Db	1329	CACACTTTGGACTCGAGCCCGGTACTCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT	1388
Qy	342	SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys	361
Db	1389	TCGCATGACAAACGGCAATCATCTCCATTCTCTTTGCTTTAGGTCGTGTCACACGGCACTAAG	1448
Qy	362	ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp	381
Db	1449	CCGCTATCTACCACGACCGTGGAGAAATCACCCAGACAGATGGATTCTCGTCTGCTTG	1508
Qy	382	ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu	401
Db	1509	ACGGTTCGGTTTGCTTCGCTTTGTACGTCGAGATGATGCACTCTCAGGCGGACAGAG	1568
Qy	402	ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp	421
Db	1569	CCGCTGTCGGTGTCTTGGTTATGATCGGTTGTCCCGCTGCATGGGTGTCCGGTTGAT	1628
Qy	422	AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly	441
Db	1629	GCITTTGGGAGATGATACCCGGGATAGCTTTGTAGGGGGTTGAGCTTTGCTAGATCTGGG	1688
Qy	442	GlyAspTrpAlaGluCysPheAla	449
Db	1689	GGTGATTGGGCGGAGTGTTTTGCT	1712
RESULT 9			
US-07-923-724-7			
; Sequence 7, Application US/07923724			
; Patent No. 5780292			
; GENERAL INFORMATION:			
; APPLICANT: Nevalainen, Helena K.M.			
; APPLICANT: Palohelmo, Marja T.			
; APPLICANT: Miettinen-Oinonen, Arja S.K.			
; APPLICANT: Torkkeli, Tuula K.			
; APPLICANT: Cantrell, Michael			
; APPLICANT: Piddington, Christopher S.			
; APPLICANT: Rambosek, John A.			
; APPLICANT: Turunen, Marja K.			
; APPLICANT: Fagerstr m, Richard B.			
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes			
; TITLE OF INVENTION: in Trichoderma			
; NUMBER OF SEQUENCES: 66			
; CORRESPONDENCE ADDRESS:			
; ADDRESS: Sterne, Kessler, Goldstein & Fox			
; STREET: 1100 New York Avenue, Suite 600			

CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/923,724
 FILING DATE: 31-JUL-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/496,155
 FILING DATE: 19-MAR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/044,077
 FILING DATE: 29-APR-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: UK 8610600
 FILING DATE: 30-APR-1986
 ATTORNEY/AGENT INFORMATION:
 NAME: Gimbala, Michele A.
 REGISTRATION NUMBER: 33,851
 REFERENCE/DOCKET NUMBER: 1050.0240004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2363 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: both
 FEATURE:
 NAME/KEY: CDS
 LOCATION: join(404..447, 550..1906)
 US-07-923-724-7

Alignment Scores:
 Pred. No.: 7,15e-270 Length: 2363
 Score: 2309.00 Matches: 436
 Percent Similarity: 99.11% Conservative: 8
 Best Local Similarity: 97.32% Mismatches: 4
 Query Match: 97.92% Indels: 0
 DB: 1 Gaps: 0

US-10-089-364-4 (1-449) x US-07-923-724-7 (1-2363)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 DB 563 CTGGCAGTCCCGGCTCGAGAAATCAATCCACTTGCAGATCGGTCAATCAGGATATCAA 622
 QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 DB 623 TGCCTTCTCCGAGACTTCGATCTTTGGGGTCAATACGGCGCGTCTTCTCTCGGCAAC 682
 QY 42 GluSerValIleSerProGluValProHlaGlyCysArgValThrPheAlaGlnValLeu 61
 DB 683 GAATCGGCGCATCTCCCTCGATGTGCGCCCGGTTGCAGAGTCATCTTCGCTCAGGTCTCTC 742
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
 DB 743 TCCCGTATGAGCGCGGTATCCGACCGAGTCCAGGGCAGAAATATCCGCTCTCAAT 802
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 DB 803 GAGGAGATCCAGCAGACGTCACCACTTTGATGGAAATATGCTTCTCTCGAGACATAC 862
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluValAsnSer 121
 DB 863 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAGCAGGAGTATGTCAACTCC 922

QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 DB 923 GGCATCAAGTTCTACAGCATGAGAAATCGCTCAAGGAAATCATCATTCGTTTCATCCGA 982
 QY 142 SerSerGlySerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 DB 983 TCCTCTGGCTCCAGCGCGTGTATCGCTCCGGCGAGAAATTCATTTGAGGGCTTCCAGAGC 1042
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 DB 1043 ACCAAGCTGAAGGATCTCTGTCGCCAGCGGGCCAAATCGTCCCAAGATCCAGCTGGTTC 1102
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 DB 1103 ATTCGAGGGCAGCTCATCCAAACACTCTCGACCCAGGCACCTGCACTGCTCTTTGAA 1162
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 DB 1163 GACAGCGAATTTGGCGATACCGTGAAGCCAAATTTACCGCCACGTTCCGCCCTCCATT 1222
 QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 DB 1223 CGTCAACGCTCGAGAACGACCTGTCTGGCGTGAATCTCTCACAGACACAGAAAGTGACCTAC 1282
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrThrValAspThrLysLeuSer 261
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 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 DB 1343 CCCTTCTGTGACCTGTTCAACCATGAGATGGAATCCACTACGACTACTCTCCAGTCCCTG 1402
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 DB 1403 AAAAAAATACTACGGCCATGGCGCAGGTAAACCGCTCGCGCCGACCCAGCGGTTCGGCTAC 1462
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 DB 1463 GCTAACGAGCTCATCGCCCTCTCAACCATCGCTCTCCACGATGATGACACGCTCCAAAC 1522
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 DB 1523 CACACCTTTGGACTCGAACCCAGTACTTCCCGCTCAACTCTACTCTCTACGCGGACTTT 1582
 QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 DB 1583 TCCACGATAACGGCATCATCTCTATCTCTTTGCTTTGGGTCTGTACACGCGCACTAAG 1642
 QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
 DB 1643 CCGTGTCTACACGACCGTGGAGAAATATACCCAGACAGATGGGTCTCTGCTGCTTGG 1702
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 DB 1703 ACGGTTCGTTTGTCTCGGCTCTGTACGTCAGATGATGAGTCCAGTCCAGGCCGAGCAG 1762
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 DB 1763 CCGTGTGCTCGTGTCTTGGTTAATGATCGCTTCTCGCGTGTGATGGGTGTCCAATTGAT 1822
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 DB 1823 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGGTGTGAGCTTTGTAGATCTGG 1882
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 DB 1883 GGTGATTGGCGGAGTGTCTGCT 1906

RESULT 10

US-08-609-426A-7
 ; Sequence 7, Application US/08609426A
 ; Patent No. 5830733

GENERAL INFORMATION:
 APPLICANT: Nevalainen, Helena K.M.
 APPLICANT: Paloheimo, Marja T.
 APPLICANT: Miettinen-Oinonen, Arja S.K.
 APPLICANT: Torkkeli, Tuula K.
 APPLICANT: Cantrell, Michael
 APPLICANT: Piddington, Christopher S.
 APPLICANT: Ramosek, John A.
 APPLICANT: Turunen, Marja K.
 APPLICANT: Fagerstr m, Richard B.
 APPLICANT: Houston, Christine S.
 TITLE OF INVENTION: Production of Phytase Degrading Enzymes
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 01-MAR-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/923,724
 FILING DATE: 31-JUL-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/496,155
 FILING DATE: 19-MAR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/044,077
 FILING DATE: 29-APR-1987

APPLICATION NUMBER: UK 8610600
 FILING DATE: 30-APR-1986
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Grant E.
 REGISTRATION NUMBER: P-41,264
 REFERENCE/DOCKET NUMBER: 1050.0080001

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2363 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: both

FEATURE:
 NAME/KEY: CDS
 LOCATION: join(404..447, 550..1906)
 US-08-609-426A-7

Alignment Scores:
 Pred. No.: 7,15e-270 Length: 2363
 Score: 2309.00 Matches: 436
 Percent Similarity: 99.11% Conservative: 8
 Best Local Similarity: 97.32% Mismatches: 4
 Query Match: 97.92% Indels: 0
 DB: 2 Gaps: 0

US-10-089-364-4 (1-449) x US-08-609-426A-7 (1-2363)

Qy 2 LeuAlaValProAlaSerArgAsnGlnSerCysAspThrValAspGlnGlyTyrGln 21
 Db 563 CTGGCAGTCCCGCGCTCGAGAAATCAATCCACTTGGATCGGTCGATCAAGGGTATCAA 622

22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 623 TGCCTTCTCGAGACTTGCATCTTTGGGGTCAATAGCGCGCTTCTTCTCTGCGCAAC 682
 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 683 GAATCGGCCATCTCCCTGATGTGCCGCGGGTTGCAGAGTCACTTTCGCTCAGGTCTC 742
 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
 743 TCCGTCATGAGCGCGGTATCCGACCGAGTCCAGGGCAAGAAATACCTCCGCTCTCAT 802
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 803 GAGGAGATCCAGCAACGCTGACCCTTTGATGGAATAATATGCCCTCTCTGAAGACATAC 862
 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGlnGlnLeuValAsnSer 121
 863 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGAGAGCAGAGCTAGTCAACTCC 922
 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 923 GGCATCAAGTTCTACCCAGCGATACGAATCGCTCACAAGGAACATCAITCCGTTTCATCGA 982
 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 983 TCCCTCTGGCTCCAGCGCGGTGATCGCTCGGGGAGAAATTCATTGAGGGCTTCCAGAGC 1042
 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 1043 ACCAAGCTGAAGGATCTCGTGCAGCGGGCCAATCGTCGCCCAAGATCGACGTGGTC 1102
 182 IleSerGluAlaSerSerSerSerSerSerLeuAspProGlyThrCysThrValPheGlu 201
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 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
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 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
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 1283 CTATGGACATGTGCTCTTCGACACCATCTCCACACGACCGCTCGACACCAAGCTGTCC 1342
 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 1343 CCCTTCTGTGACCTGTTCCACCATGACGAATGGATCCACTACCTACCTCCAGTCCCTG 1402
 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 1403 AAAAAATACTACGCCCATGTGCGCAGGTAAACCCCTCGGCCGCCACCCAGGGCGTGGGTAC 1462
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 1463 GCTAACGAGCTCATGCCCGCTCTACCCACTCGCCTGTCCCGATGACACACAGCTCCAAC 1522
 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
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QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGln 401
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QY 442 GlyAspTrpAlaGluCysPheAla 449
Db 1883 GGTGATTGGGCGGAGTGTCTGTCT 1906

RESULT 11

US-08-374-652C-1
; Sequence 1, Application US/08374652C
; Patent No. 5834286
; GENERAL INFORMATION:
; APPLICANT: NEVALAINEN, HELENA K.M.
; APPLICANT: PALOHEIMO, MARJA T.
; APPLICANT: FAGERSTROM, RICHARD B.
; APPLICANT: MIETTINEN-OINONEN, ARJA S.
; APPLICANT: TURUNEN, MARJA K.
; APPLICANT: RAMBOSEK, JOHN A.
; APPLICANT: PIDDINGTON, CHRISTOPHER S.
; APPLICANT: HOUSTON, CHRISTINE S.
; APPLICANT: CANTRELL, MICHAEL A.
; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
; TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
; TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,652C
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/925,401
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, GRANT E.
; REGISTRATION NUMBER: 41,264
; REFERENCE/DOCKET NUMBER: 1050.071001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

; NAME/KEY: CDS
; LOCATION: Join(404...447, 550...1906)
US-08-374-652C-1
Alignment Scores:
Pred. No.: 7.23e-270 Length: 2379
Score: 2309.00 Matches: 436
Percent Similarity: 99.11% Conservative: 8
Best Local Similarity: 97.32% Mismatches: 4
Query Match: 97.92% Indels: 0
DB: Gaps: 2
US-10-089-364-4 (1-449) x US-08-374-652C-1 (1-2379)
QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db 579 CTGGCAGTCCCGCCTCGAGAAATCAATCCACTTCGATACGTCGATCAAGGTATCAA 638
QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db 639 TGCCTTCTCGAGACTTCGATCTTTGGGGTCAATACGGGCCCTTTCTCTCTGGCAAC 698
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 699 GAATCGGCCATCTCCCTCTGATGTCGCCCGCTTCAGAGTCACCTTCGCTCAGGTCCTC 758
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
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QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
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QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db 879 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAGCAGGASCTAGTCAACTCC 938
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 939 GGCATCAAGTTCTACCAGCGATACGATCGCTCAACAGAAACATCATTCGCTTCATCGGA 998
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db 999 TCCTCTGCTCCAGCCGGTGATGCGCTCCGGCAGAAATTCATTGAGGGCTTCAGAGC 1058
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 1059 ACCAAGCTGAAGGATCCTCGTCCCGCCAGCCGCAATCGTCGCCCAAGATCGAGCTGTC 1118
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
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Db 1179 GACAGCGAATGGCCGATACCGTCAAGCCCAATTTACCGCCAGCTTCGCCCTTCCAA 1238
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db 1239 CGTCAAGCTCTGGAGAACGACCTGTCTGGCGTGATCTCTCAGACACAGAAAGTGACCTAC 1298
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db 1299 CTCATGACATGTGCTCTCTTCGACCATCATCTCCACAGCAGCCGTCGACACCAAGCTGCC 1358
QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db 1359 CCCTTCTGTGACCTGTTTCACCCATGAGAAATGGATCCACTACGACTACCTCCAGTCCCTG 1418
QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
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Qy	302	AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn	321
Db	1479	GCTAAAGAGCTCATCGCGCGTCTCACCACTCGCTGTCCACGATGACACCACTCCAAC	1538
Qy	322	HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyAlaAspPhe	341
Db	1539	CACACCTTGAGCTCGAACCCAGCTACCTCCCGCTCAACTCTACTCTCTACGGCGACTTT	1598
Qy	342	SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyAsnGlyThrLys	361
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Db	1659	CCGCTGTCCTACACGACCGTGGAGATATCACCCAGACAGATGGTTCTCGTCTGCTTG	1718
Qy	382	ThrValProPheAlaSerArgLeuTyValGluMetMetGlnCysGlnAlaGluGlnGlu	401
Db	1719	ACGGTTCCGTTTGCTTCGGTCTGTACGTCGAGATGATGCACTGCCAGGCCGAGCAGAG	1778
Qy	402	ProLeuValArgValLeuValAlaAsnAspArgValValProLeuHisGlyCysProValAsp	421
Db	1779	CCGCTGGTCCGTGTCCTTGGTTAATGATCGCGTGTCCCGCTGCCATGGGTGTCCAATTGAT	1838
Qy	422	AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly	441
Db	1839	GCCTTGGGGAGATGATCCCGGGATAGCTTTGTGAGGGGGTGTGACTTTGCTAGATCTGGG	1898
Qy	442	GlyAspTrpAlaGluCysPheAla	449
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RESULT 12

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US-09-155-855-5
; Sequence 5, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155, 855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(45)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (157)..(183)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (184)..(1512)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
; US-09-155-855-5

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Alignment Scores:	1,95e-266	Length:	1515
Pred. No.:	2278.00	Matches:	427
Score:	98.44%	Conservative:	14
Percent Similarity:	95.31%	Mismatches:	7
Best Local Similarity:	96.61%	Indels:	0
Query Match:	3	Gaps:	0
DB:			
US-10-089-364-4 (1-449) x US-09-155-855-5 (1-1515)			
Qy	2	LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln	21
Db	169	CTGGCAGTCCCGCCCTCGAAGATCAATCCACTTCGGATACGGTGCATCGAGGGGTATCAA	228
Qy	22	CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn	41
Db	229	TGCTTCGGAGACTTCGCATCTTTGGGGCCAAATACGGCCGCTCTTTCTCTGGCAAC	288
Qy	42	GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu	61
Db	289	AAATCGCCCATCCTCCCTCATGTTCTTCGGATGCCATGTCACATTTGCCACGGTTC	348
Qy	62	SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle	81
Db	349	TCCGGCATTGGACACGGTATCCGACCGACTCAAGGGCAAGAAATACTCGCTCTCATC	408
Qy	82	GluGluIleGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuIleYsThrTyr	101
Db	409	GAGGAGATCCAGCAGAAACGACACTTCGAGGGGAAATATGCTTCTCGAAGACATAC	468
Qy	102	AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSer	121
Db	469	AACCTACAGCTGGGCGGATGATCTGCTCCCTTCGGAGACGAGAGCTGTCACCTCC	528
Qy	122	GlyTLeLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg	141
Db	529	GGCGTCAAGTCTTACAGCGATACGATCGCTCACAAGAAACATTTGTCCTCATCCGA	588
Qy	142	SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer	161
Db	589	TCCTCAGGCTCCAGCGCGTGAITGGCTCTGGCAATAAATTCATCGAGGGCTTCAGAGC	648
Qy	162	ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal	181
Db	649	ACTAAGCTGAAGGATCTCTGTGCTCCAGCCGGCCAAATCGTCCGCCAAGATCCACGTGTC	708
Qy	182	IleSerGluAlaSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu	201
Db	709	ATTTACAGGCCACGACATCCACACACTCTCGATCCGGGACCTGCACCGTTTTCGAA	768
Qy	202	AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle	221
Db	769	GATAGCGAAATGGCCGATGATACGAGAGCAATTTCCCGCCACGCTGCTCCCTCCATT	828
Qy	222	ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr	241
Db	829	CGTCAACGCTCGAGAGACGACTTGTCTGGCGTGTCTCTACGGACACACAGATGACCTAC	888
Qy	242	LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer	261
Db	889	CTCATGGACATGCTCTCTTCGACACCATCTCCACGACCGCTCGACACCAAGCTGTCC	948
Qy	262	ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu	281
Db	949	CCCTTCTGTGACCTGTTCACCCATAGAGAAATGATCACTACACACTTCACCTCCAGTCCCCG	1008
Qy	282	LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr	301
Db	1009	AACAAATACTAGGCCATGGCGCAGGTAAACCCGCTCGGCCCGACCCAGGGCGTCTGCTAC	1068
Qy	302	AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn	321

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Db      1069 GCTAACGAGCTCATGCCCGCTCTCAACCCACTCGCTGTCTCCAGATGACACACCGCTCCAAC 1128
Qy      322 HistThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db      1129 CACACATTTGGACTCCAAACCGGCTACTTTCCCGCTCACTCCACTCTCTATCGGACTTT 1188
Qy      342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db      1189 TCGCATGATAACGGCATCATCTCTATCCCTCTTTTGGTCTGTATACAAACGGCACCAG 1248
Qy      362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
Db      1249 CGCGTGTCTTTCACACCGCGGAGAAATATCACCCAGACGATGGGTCTCTCATCTCGCTGG 1308
Qy      382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db      1309 AGGGTTCCTTTCGCGCTCGGCGATGTACGTGAGATGATGCAATGCGAGTCCGAGCAGGAG 1368
Qy      402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db      1369 CTTTGGTCCGTGTCTGTGTTAATGATCGTGTGTTCGCTGCATGGCTGTCCGGTTGAT 1428
Qy      422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db      1429 GCTTTGGGAGAGATGACCGCGGATAGCTTCGTGAAGGGGTTGAGCTTTGCCAGATCTGGC 1488
Qy      442 GlyAspTrpAlaGluCysPheAla 449
Db      1489 GGTGATTTGGGGGAGTGTTCGCT 1512

RESULT 13
US-09-543-744-5
; Sequence 5, Application US/09543744
; Patent No. 6309870
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/543,744
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(45)
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; NAME/KEY: sig_peptide
; LOCATION: (157)..(183)
; NAME/KEY: mat_peptide
; LOCATION: (184)..(1512)
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
US-09-543-744-5

Alignment Scores:
Pred. No.: 1.95e-266 Length: 1515
Score: 2278.00 Matches: 427
Percent Similarity: 98.44% Conservative: 14
Best Local Similarity: 95.31% Mismatches: 7
Query Match: 96.61% Indels: 0

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DB:      3      0      Gaps:
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Qy      2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db      169 CTGGCAGTCCCGCGCTCGAGAAATCAATCCACTTCGATACGTCGATCAGGGATATCAA 228
Qy      22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaSer 41
Db      229 TGCTTCTCGGAGACTTCGCATCTTTGGGGCCAATACGGCGCGTCTCTTTCTCTGGCAAC 288
Qy      42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db      289 AAATCGGCATCTCCCTGATGTTCTCCGATGCCATGTCTCTTTCGCCCGAGTTCTC 348
Qy      62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
Db      349 TCCGCCATCGAGCACCGGTATCCGACCGCATCCCAAGGCAAGAAATACTCCGCTCTCATC 408
Qy      82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db      409 GAGGAGATCCACGACGACACACCTTCGAGGGGAAATATGCCCTCTCTGAAGCATAC 468
Qy      102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db      469 AACTACAGCTTGGGCGCGGATGATCTGACTCCCTTCGGAGAGAGAGAGCTGGTCAACTCC 528
Qy      122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db      529 GCGCTCAAGTTCTACCGAGCATACGAATCGCTCAAGAAACATTTGTCCTCCGTTTCAATCGA 588
Qy      142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161
Db      589 TCCTCAGGCTCCAGCGCGTGATTCCTCTGGCAATAAATTCATCGAGGGGTTCAGAGC 648
Qy      162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db      649 ACTAAGCTGAAGGATCTCTGTCGCCAGCCCGCCCAATCGTCCCAAGATCGACGTGTC 708
Qy      182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db      709 ATTTCAGAGGCCAGCACATCCAAACAACACTCTCGATCCGGCACCTGCACCGTTTCGAA 768
Qy      202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db      769 GATAGCGAATTTGGCCGATGATCAAGAGCAATTTCAACCGCACGTTTCCTCCCTCCATT 828
Qy      222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db      829 CGTCAACGTCTGGAGAGAGCTTGTCTGGCGTGCTCTCTCAGGACACAGAGTGACCTTAC 888
Qy      242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db      889 CTCATGGACATGTGCTCTCTCGACCACTCTCCACGACCGTCGACACCAAGCTGTCC 948
Qy      262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db      949 CCCTTCTGTGACCTGTTCACCCATGAAGATGGATCAACTACGACTACCTCCAGTCCCTG 1008
Qy      282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db      1009 AACAAATACTACGGCCATGGCGAGGTAAACCGCTCGCGCCGACCCAGGGGCTCGGTAC 1068
Qy      302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db      1069 GCTAACGAGCTCATCGCCCGCTCTCACCACTCGCTCTCCAGATGACACACCGCTCCAAC 1128
Qy      322 HistThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db      1129 CACACATTTGGACTCCAAACCGGCTACTTTCCCGCTCACTCCACTCTCTATGCGGACTTT 1188
Qy      342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361

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QY 362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
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QY 382 ThrValProPheAlaSerArgLeuThrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db 1309 ACGGTTCTTTCCGCTCGGCGATGTACGTGAGATGATCAATGCCAGTCCGAGCAGGAG 1368
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db 1369 CTTTGGTCCGTGCTGTTGTTAATGATCGTGTGTTGTTCCGCTGATGCTGCTGAT 1428
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db 1429 GCTTTGGGAAGATGTACGGGGATAGCTTCGTGAGGGGTGAGCTTTGCCAGATCTGGC 1488
QY 442 GlyAspTrpAlaGluCysPheAla 449
Db 1489 GGTGATTGGGGGAGTGTTCGCT 1512

RESULT 14
US-09-929-060-5
; Sequence 5, Application US/09929060
; Patent No. 6548282
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIDEMASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEXO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TAIJOYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
US-09-929-060-5

Alignment Scores:
Pred. No.: 1.95e-266 Length: 1515
Score: 2278.00 Matches: 427
Percent Similarity: 98.44% Conservative: 14
Best Local Similarity: 95.31% Mismatches: 7
Query Match: 96.61% Indels: 0
DB: 4 Gaps: 0

US-10-089-364-4 (1-449) x US-09-929-060-5 (1-1515)
QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTrpGln 21
Db 169 CTGGAGTCCCGCTCGAGAAATCATCCACTTGGCATAGGTCGATCAGGGGTATCAA 228
QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTrpAlaProPhePheSerLeuAlaAsn 41
Db 229 TGCCTCTCGGAGACTTCGCACTTTGGGGCCAAATACGCGCGCTTCTTTCTCTGCGCAAAC 288
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QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 289 AAATGGCCATCTCCCTGATGTTCTGCGGATGCCATGTTCATCTGCCAGGTTCTC 348
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaIle 81
Db 349 TCCCGCCATGGAGCAGGTATCCGACCGACTCCAAGGCGAAGAAATATCTCCGCTCTCATC 408
QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 409 GAGGAGATCCAGCAAGACCGACACCTTCGAGGGGAAATATGCCCTTCTGAGACATAC 468
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSer 121
Db 469 AACTACAGCTGGCGCGGATGATCTGACTCCCTTCGGAGAGCAGGAGTGGTCAACTCC 528
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 529 GCGCTCAAGTTCTACCCAGCGATACGAATCGCTCACAGAAACATTCGCCGTTTCATCCGA 598
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db 589 TCCTCAGGCTCCAGCGCGTGATTGCTCTGGCAATAAATTCAFCAGGGCTTCAGAGC 648
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 649 ACTAAGCTGAGGATCTCTGTCGCCAGCGGCCAATCGTCGCCAAGATCGACGTGGTC 708
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db 709 ATTTCAAGGCCAGCACATCCAAACACTCTCGATCCGGGCACCTGCACCGTTTCGAA 768
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db 769 GATAGCGAATTGGCCGATGACATCGAAGCCAAATTCACGCCACGTTCTGTCCTCCATT 828
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db 829 CGTCAACGCTGGAGAACGACTTGTCTGGCGTCTCTCACGGACACAGAAAGTACCTAC 888
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db 889 CTCATGGACATGTGCTCTTCGACACCATCTCCACCAGCACCGTCGACACCAAGCTCTCC 948
QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db 949 CCCTTCTGTGACCTGTTTACCCATGAAGATGATGATGATGATGATGATGATGATGATG 1008
QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db 1009 AACAAATACTACGGCCATGCGCAGGTAAACCCGTCGGCCGACCCAGGCGCTCGGCTAC 1068
QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db 1069 GCTAACGAGCTCATCGCCCGCTCTCACCCACTCGCTCTCCAGATGATGATGATGATGATGAT 1128
QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db 1129 CACATGTGACTCCAAACCGGCTACTTTCCGCTCAACTCCACTCTCTATGCGGACTTT 1188
QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db 1189 TCGCATGATAAGGCAATCATCTCTATCTCTTTGCTTGGGTCTGTGTAAACAGGCGACCAAG 1248
QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db 1249 CCGTGTCTTCCACGACCGCGGAGAAATATCAACCAGACCGATGGGTCTCATCTGCTCG 1308
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
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QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db 1369 CTTTGGTCCGTCCTTGGTTAATGATCGTTGTTCCGCTGTCATGGCTGCGGTTGAT 1428
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db 1429 GCTTTGGGAGAGTACGCGGAGATAGCTTCGTGAAGGGTTGAGCTTTGCCAGATCTGCC 1488
QY 442 GlyAspTrpAlaGluCysPheAla 449
Db 1489 GGTGATTGGGGGAGTGTTCGCT 1512

RESULT 15
US-09-155-855-4
; Sequence 4, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/011175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1332)
US-09-155-855-4

Alignment Scores:
Pred. No.: 9,76e-264 Length: 1332
Score: 2255.00 Matches: 422
Percent Similarity: 98.42% Conservative: 14
Best Local Similarity: 95.26% Mismatches: 7
Query Match: 95.63% Indels: 0
DB: 3 Gaps: 0

US-10-089-364-4 (1-449) x US-09-155-855-4 (1-1332)

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QY 27 SerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGluSerValIleSer 46
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QY 47 ProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyAla 66
Db 121 CCTGATGTCCTCGGAGTGCATGTCACTTTCGCCCAAGTCTCTCCCGCATGGAGCA 180
QY 67 ArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGluGluIleGln 86
Db 181 CGGTATCCGACCGACTCCAGGGGGAATATACCTCCGCTCTCATCGAGGAGATCCAGCAG 240
QY 87 AsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsnTyrSerLeuGly 106
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QY 107 AlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGlyIleLysPheTyr 126

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Search completed: October 24, 2004, 17:26:17
Job time : 175 secs

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QY 127 GlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSerSerGlySerSer 146
Db 361 CAGCGATACGAATCGCTCACAAGAACATTTGTCGCGTTTCATCCGATCTCTCAGGCTCCAGC 420
QY 147 ArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLysLeuAsp 166
Db 421 CGCGTGATGCTCTGGCAATTAATTCATCGAGGGCTTCCAGAGCACTAAGCTGAAGGAT 480
QY 167 ProArgAlaGlnProGlyGlnSerSerProLysIleAspValIleSerGluAlaSer 186
Db 481 CCTCGTCCAGCCCGGCCAATCGTCGCCCAAGATCGAGCTGGTTCATTTTCAGAGGCCAGC 540
QY 187 SerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAspSerGluLeuAla 206
Db 541 ACATCCAAACACACTCTCGATCCGGGCACCTGCACCGCTTCGAAAGATAGCAATTTGGCC 600
QY 207 AspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArgGlnArgLeuGlu 226
Db 601 GATGACATCGAAGCCAAATTCACCGCCACGTTCTGTCCTCCATTCGTCACGCTCTGGAG 660
QY 227 AsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeuMetAspMetCys 246
Db 661 AACGACTTGTCTGGGCTGTCTCTCACGGACACAGAAAGTGACCTACTCATGGACAATGTC 720
QY 247 SerPheAspThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspLeu 266
Db 721 TCCITTCGACACCATCTCCACGACGACCGTCGACACCAAGCTGTCCCTCTCTGTGACCTG 780
QY 267 PheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLysLysTyrTyrGly 286
Db 781 TTCACCCATGAAGATGGATCAACTACGACTACTCTCCAGTCCCTGAAACAATACTACGGC 840
QY 287 HisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAlaAsnGluLeuIle 306
Db 841 CATGGCGCAGGTAACCCGCTCGGCCGACCCAGGGCGTCGGCTACGCTAACGAGCTCATC 900
QY 307 AlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHisThrLeuAspSer 326
Db 901 GCCCGTCTCACCCACTCGCTGTCCAGATGACACACAGCTCCAAACACACATTTGGACTCC 960
QY 327 SerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGly 346
Db 961 AACCCGGCTACTTTCCCGCTCAATCCACTCTATGCGGACTTTTCGATGATAACGGC 1020
QY 347 IleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrThr 366
Db 1021 ATCATCTCTATCTCTTGTGTTGCTGTACAAAGGACCAAGCGCTGCTCTTCCAGC 1080
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Db 1081 ACCCGGAGAAATATCACCCAGACCGATGGGTCTCTCATCTGCTGGACGGTTCCTTTTCGCG 1140
QY 387 SerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluProLeuValArgVal 406
Db 1141 TCGCGCATGTACGTCGAGATGATCAATGCCAGTCCGAGCAGGAGCCCTTTGGTCCGCTC 1200
QY 407 LeuValAsnAspArgValValProLeuHisGlyCysProValAspAlaLeuGlyArgCys 426
Db 1201 TTGTTAATGATCGTGTGTTTCCGCTCATGGCTGTCCGGTTGATGCTTTTGGGAGATGT 1260
QY 427 ThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGlu 446
Db 1261 ACGGGATAGCTTCGTAAGGGGTTGAGCTTTGCCAGATCTGCGCGGTGATTGGGGGAG 1320
QY 447 CysPheAla 449
Db 1321 TGTTCGCT 1329

```


GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 12:59:09 ; Search time 828 Seconds
(without alignments)
2846.606 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MLAVPASRNQSSCDTVDQGY.....SFVGLSFARGGDWAECEFA 449

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134896 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=N Geneseq_23Sep04 -QWMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
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-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_23Sep04:.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2358	100.0	1350	4	AAD03283 Aspergill
2	2358	100.0	1449	4	AAD03287 Carrot ex
3	2353	99.8	1344	6	ABn85591 Aspergill
4	2353	99.8	1382	6	ABn85587 Aspergill
5	2353	99.8	1289	6	ABn85590 Aspergill
6	2353	99.8	1404	2	AAQ11175 Chromosom

7	2353	99.8	1404	2	AAZ27421	A. ficcum
8	2353	99.8	1506	6	ABn85588	Aspergill
9	2353	99.8	2665	12	ADL91241	Wild-type
10	2353	99.8	6756	2	AAQ11174	Sequence,
11	2353	99.8	6756	2	AAT65137	Aspergill
12	2353	99.8	6756	8	ABX13436	Plasmids
13	2350	99.7	1344	6	ABn85592	Aspergill
14	2350	99.7	2665	12	ADL91267	Mutant ph
15	2350	99.7	2665	12	ADL91261	Mutant ph
16	2349	99.6	2665	12	ADL91263	Mutant ph
17	2349	99.6	2665	12	ADL91247	Mutant ph
18	2349	99.6	2665	12	ADL91259	Mutant ph
19	2349	99.6	2665	12	ADL91257	Mutant ph
20	2348	99.6	2665	12	ADL91273	Mutant ph
21	2348	99.6	1404	2	AAT65136	Aspergill
22	2347	99.5	2665	12	ADL91255	Mutant ph
23	2347	99.5	2665	12	ADL91271	Mutant ph
24	2347	99.5	2665	12	ADL91269	Mutant ph
25	2347	99.5	2665	12	ADL91245	Mutant ph
26	2346	99.5	2665	12	ADL91251	Mutant ph
27	2346	99.5	2665	12	ADL91279	Mutant ph
28	2346	99.5	2665	12	ADL91265	Mutant ph
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30	2345	99.4	2665	12	ADL91275	Mutant ph
31	2343	99.4	2665	12	ADL91277	Mutant ph
32	2343	99.4	2665	12	ADL91308	Mutant ph
33	2342	99.3	2665	12	ADL91283	Mutant ph
34	2341	99.3	1404	2	AAQ13878	Phytase g
35	2341	99.3	2665	12	ADL91291	Mutant ph
36	2341	99.3	2665	12	ADL91289	Mutant ph
37	2340	99.2	2665	12	ADL91293	Mutant ph
38	2339	99.2	2665	12	ADL91287	Mutant ph
39	2339	99.2	2665	12	ADL91285	Mutant ph
40	2327	98.7	2665	12	ADL91295	Mutant ph
41	2309	97.9	2363	2	AAQ58126	Phytase g
42	2309	97.9	2379	2	AAQ56944	A. niger
43	2277	96.6	1350	4	AAQ03282	Aspergill
44	2277	96.6	1449	4	AAQ03286	Carrot ex
45	2268	96.2	1590	12	ADK90935	Aspergill

ALIGNMENTS

RESULT 1	
AAD03283	
ID	AAD03283 standard; DNA; 1350 BP.
XX	
AC	AAD03283;
DT	13-JUN-2001 (first entry)
DE	Aspergillus niger phytase (Phy) A-1 gene.
XX	
KW	Phytase A; Phy; plant productivity; phosphorus utility;
KW	biomass production; hypocotyl production; epicotyl production;
KW	transgenic plant; phytate; ds.
XX	
OS	Aspergillus niger.
XX	
PH	Key
FT	Location/Qualifiers
FT	1..1350
FT	/*tag= a
FT	/product= "Aspergillus niger phytase A-1 protein"
XX	
PN	WO200122806-A1.
XX	
PD	05-APR-2001.
XX	
PF	22-SEP-2000; 2000WO-AU001183.
XX	
PR	24-SEP-1999; 99AU-00003049.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.

PA (AUWO-) AUSTRALIAN WOOL RES & PROMOTION ORG.
 XX Richardson AE, Hayes JE, Simpson RJ;
 XX P-PSDB; AAY72974.
 DR WPI; 2001-244964/25.
 DR P-PSDB; AAY72974.
 XX
 XX
 PT New isolated nucleic acid encoding a mature phytase polypeptide for
 PT enhancing the phosphorus nutrition of a plant, the growth of a plant on a
 PT phosphorus source and the phosphorus content of a plant.
 XX
 XX Claim 7; Page 121-124; 144pp; English.
 PS
 XX The invention relates to a method of modifying plant productivity which
 CC involves expressing phytase (Phy) A gene from *Aspergillus niger*, in a
 CC plant cell. Phytase gene is capable of facilitating plants ability to
 CC utilise soil phosphorus. It is used to enhance the phosphorus nutrition
 CC of a plant or the growth of a plant on a phosphorus source comprising
 CC phytate and/or increase the phosphorus content of a plant. This gene is
 CC used to enhance the biomass produced by a plant and also to enhance the
 CC rate of hypocotyl production or the rate of epicotyl production.
 CC transgenic plant containing phytase gene has improved productivity than
 CC its isogenic counterparts. The present sequence is *Aspergillus niger* Phy
 CC A-1 gene. This gene is modified (Phy A-2 gene) in order to bring about
 CC suitable expression in plant cells
 XX
 SQ Sequence 1350 BP; 288 A; 419 C; 332 G; 311 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5,53e-235 Length: 1350
 Score: 2358.00 Matches: 449
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-089-364-4 (1-449) x AAD03283 (1-1350)

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 DB 1 ATGCTGGAGTCCCGCCCTCGAAGAAATCAATCCAGTTGGCATACGGTCGATCGAGGGTAT 60
 QY 21 GlnCysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAla 40
 DB 61 CAAATGCTCTCCGAGACTTGGCATCTTGGGGTCAATACGACCGGTTCTCTCTGGCA 120
 QY 41 AsnGluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnVal 60
 DB 121 AACGAATCGGTATCTCCCTGAGGTGCGCGCGGATGCGAGTCACTTTTCGCTCAGGTC 180
 QY 61 LeuSerArgHisGlyAlaArgTyrProThrAspSerIlysglyLysTyrSerAlaLeu 80
 DB 181 CTCTCCCGTCATGAGCGCGGTATCCGACCGATCCAAAGGCGAAGAAATCTCCGCTCTC 240
 QY 81 IleGluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThr 100
 DB 241 ATTGAGGAGTCCAGCAGAAGCGGACCCACTTTGACGGAAATATGCTTCTTGAAGACA 300
 QY 101 TyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsn 120
 DB 301 TACAACCTACAGCTTGGGTGAGATGACCTGACTCCCTTCGAGAACAGAGGAGCTAGTCAAC 360
 QY 121 SerGlyLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIle 140
 DB 361 TCCGGCATCAAGTCTTACAGCGGTACGAATCGCTCACAGGAACATCGTTCCATTCATC 420
 QY 141 ArgSerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGln 160
 DB 421 CGATCTCTGGTCCAGCGCGGTATCCGCTCCGGCAAGAAATTCATCGAGGGGCTTCCAG 480
 QY 161 SerThrIlyLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspVal 180
 DB 481 AGCACCAGCTGAAGGATCTCTCGTGGCCAGCCCGGCCAATCGTCGCCCAAGATCGACGTG 540

181 ValIleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPhe 200
 DB 541 GTCATTTCCGAGGCGAGCTCATCCAAACACACTTCGAGCCAGGACCTGCACTGTCTTC 600
 QY 201 GluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSer 220
 DB 601 GAAGACAGCGAATTTGGCCGATACCGTCGAAGCAATTTACCGGCCAGTTCGTCCTCCCTCC 660
 QY 221 IleArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThr 240
 DB 661 ATTCGTCAACGTCCTGGAGAACGACCTGTCGGTGTGACTCTCACAGACACAGAGTGACC 720
 QY 241 TyrLeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeu 260
 DB 721 TACCTCATGGACATGTGCTCTTCGACACCATCTCCACGACCCGCTCGACACCAAGCTG 780
 QY 261 SerProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSer 280
 DB 781 TCCCCCTTCTGTGACCTGTTCCATCCCATGACGAATGGATCAACTACGACTACCTCCAGTCC 840
 QY 281 LeuLysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGly 300
 DB 841 TTGAAAAGATATTACGGCCATGTGTGAGTAAACCCGCTCGGCCGACCCAGGGCGTTCGGC 900
 QY 301 TyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSer 320
 DB 901 TAGGCTAACGAGCTCATCGCCGCTCTGACCCACTCGCCTGTCCACGATGACACCAAGTTC 960
 QY 321 AsnHisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAsp 340
 DB 961 AACCACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGAC 1020
 QY 341 PheSerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThr 360
 DB 1021 TTTTCGATGACAAACGGCATCACTCCATCTCTTTGCTTTAGTCTGTACAAACGGCACT 1080
 QY 361 LysProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAla 380
 DB 1081 AAGCCGCTATCTACCAAGCCGTCGGAGAAATATCAACCCAGACAGATGGATTCTCGTCTGT 1140
 QY 381 TrpThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGln 400
 DB 1141 TGGACGGTTCCGTTTCTGCGGTTTGTACGTGAGATGATGATGATGATGATGATGATGATG 1200
 QY 401 GluProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProVal 420
 DB 1201 GAGCCGCTGCTCGGTGCTTGGTTAATGATCGCGTGTTCGCCGTGATGGGTGTCGGTT 1260
 QY 421 AspAlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSer 440
 DB 1261 GATGCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTGTGATGATCT 1320
 QY 441 GlyGlyAspTrpAlaGluCysPheAla 449
 DB 1321 GGGGGTCAATGGCGGAGTGTGTTTGTCT 1347

RESULT 2
 AAD03287
 ID AAD03287 standard; DNA; 1449 BP.
 XX
 AC AAD03287;
 XX
 XX 11-SEP-2003 (revised)
 DT 13-JUN-2001 (first entry)
 XX
 DE Carrot extensin leader peptide-A. niger phytase A-1 chimeric gene.
 XX
 KW Phytase A; Phy; plant productivity; phosphorus utility;
 KW biomass production; hypocotyl production; epicotyl production;
 KW transgenic plant; phytate; carrot; extensin; ds.
 XX
 OS *Daucus carota*.

OS Aspergillus niger.
 XX Chimeric.

Key Location/Qualifiers
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 phytase A-1 chimeric protein"
 sig_peptide 1..100
 /tag= b
 /note= "Carrot extensin leader peptide"
 mat_peptide 101..1446
 /tag= c
 /product= "Mature carrot extensin leader peptide- A.
 niger phytase A-1 chimeric protein"
 WO200122806-A1.
 05-APR-2001.
 22-SEP-2000; 2000WO-AU001183.
 24-SEP-1999; 99AU-00003049.
 (CSIR) COMMONWEALTH SCI & IND RES ORG.
 (AUWO-) AUSTRALIAN WOOL RES & PROMOTION ORG.
 Richardson AE, Hayes JE, Simpson RJ;
 WPI: 2001-244964/25.
 P-PSDB; AAY72978.
 New isolated nucleic acid encoding a mature phytase polypeptide for
 enhancing the phosphorus nutrition of a plant, the growth of a plant on a
 phosphorus source and the phosphorus content of a plant.
 Claim 9; Fig 1; 144pp; English.

The invention relates to a method of modifying plant productivity which
 involves expressing phytase (Phy) A gene from Aspergillus niger, in a
 plant cell. Phytase gene is capable of facilitating plants ability to
 utilise soil phosphorus. It is used to enhance the phosphorus nutrition
 of a plant or the growth of a plant on a phosphorus source comprising
 phytate and/or increase the phosphorus content of a plant. This gene is
 used to enhance the biomass produced by a plant and also to enhance the
 rate of hypocotyl production or the rate of epicotyl production.
 Transgenic plant containing phytase gene has improved productivity than
 its isogenic counterparts. The present sequence is carrot extensin leader
 peptide-A. niger phytase A-1 chimeric gene. This chimeric gene is used to
 enhance phosphorus nutrition in plants. (Updated on 11-SEP-2003 to
 CC standardise OS field)

XX Sequence 1449 BP; 312 A; 439 C; 355 G; 343 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 6,14e-235 Length: 1449
 Score: 2358.00 Matches: 449
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-089-364-4 (1-449) x AAD03287 (1-1449)

QY 1 MetLeuAlaValProAlaSerArgGlnSerSerCysAspThrValAspGlnGlyTyr 20
 DB 100 ARGCTGGCAGTCCCGCTCGAGAATCAATCCAGTTCGATCGATCGAGGGTAT 159

QY 21 GlnCysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAla 40
 DB 160 CAATGCTTCTCGAGACTTCGACATCTTGGGGTCAATACGACACCGCTTCTCTCTGGCA 219

QY 41 AsnGluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnVal 60

DB 220 AACGAATCGGTCACTCCCTGAGGTGCCGCGGATGAGAGTCACTTCGCTCAGGTC 279

QY 61 IeuSerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeu 80

DB 280 CTTCTCCGTCATGGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATACCTCGCTCTC 339

QY 81 IleGluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThr 100

DB 340 ATTGAGGAGATCCAGCAGAACCGGACCCCTTTGACGAAATATATGCTTCTCTGAGACA 399

QY 101 TyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGlnGlnLeuValAsn 120

DB 400 TACAACATACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGGAGTAGTCAAC 459

QY 121 SerGlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIle 140

DB 460 TCCGGCATCAAGTTCTACGAGCGGTACGAATCGCTCACAAAGGAACATCGTTCCATTTCATC 519

QY 141 ArgSerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGln 160

DB 520 CGATCTCTGGGTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCCAG 579

QY 161 SerThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspVal 180

DB 580 AGCACCAAGCTGAGGATCTCTGTCGCCAGCCCGGCAATCGTCCGCCCAAGATCGACGTG 639

QY 181 ValIleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPhe 200

DB 640 GTCATTTCCGAGGCCAGCTCATCCAAACAACACTCTCGACCCAGGACCTGCATCTGCTTC 699

QY 201 GluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSer 220

DB 700 GAAGACACGGAAATGGCCGATACCGTCGAAGCAATTTACCGCCACGTTCTGTCCTCTCC 759

QY 221 IleArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThr 240

DB 760 ATTCTCAACGCTCGAGAACGACCTGTCGGTGTGACTCTCACAGACACAGAACTGACC 819

QY 241 TyrLeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeu 260

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QY 261 SerProPheCysAspLeuPheThrHisAspGluTrrIleAsnTyrAspTyrLeuGlnSer 280

DB 880 TCCCCCTTCTGTGACTGTTTACCACCAAGCAATGGAATCACTACACTACCTCCAGTCC 939

QY 281 LeuLysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGly 300

DB 940 TTGMAAAGTATTACGGCCATGGTGAGGTAAACCGCTCGGCCGACCCAGGGCGTCCGC 999

QY 301 TyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSer 320

DB 1000 TACGCTAACGAGCTCATCGCCCGTCTGACCCACTCGCTGTCCAGATGACACCACTTCC 1059

QY 321 AsnHisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAsp 340

DB 1060 AACACACTTTGGACTCGAGCCCGGCTACCTTTTCGCTCAACTCTACTCTCTACCGGAC 1119

QY 341 PheSerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyIleuTyrAsnGlyThr 360

DB 1120 TTTTCGATGACAACGGCATCATCTCCATTCTCTTTGCTTTAGGTCTGTACAACGGCACT 1179

QY 361 LysProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAla 380

DB 1180 AAGCCGCTATCTACACGACCGCGAGAAATATACCCAGACAGATGGATTCTCGTCTGCT 1239

QY 381 TrpThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGln 400

DB 1240 TGGACGGTTCCGTTGCTTCGCGTTTGTACGTGAGATGATGCAGTGTGACGGAGAGCAG 1299

QY 401 GluProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProVal 420

Db 1300 GAGCCGCTGGTCCGTCGTCCTGGTTAATGATCGGTTGTCCCGCTGCATGGGTCTCCGGTT 1359
 QY 421 AspAlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSer 440
 Db 1360 GATGCTTTGGGAGAGTATCCCGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCT 1419
 QY 441 GlyGlyAspTrpAlaGluCysPheAla 449
 Db 1420 GGGGGTGAATTGGCGGAGTGTTTGTCT 1446
 RESULT 3
 AEN85591
 ID AEN85591 standard; DNA; 1344 BP.
 AC AEN85591;
 XX AEN85591;
 XX
 DT 17-SEP-2002 (first entry)
 XX
 DE Aspergillus niger phyA related polynucleotide 4.
 XX
 KW Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; gene; ds.
 XX
 OS Aspergillus niger.
 XX
 PN CM133363-A.
 XX
 XX 30-JAN-2002.
 PD
 PF 12-JUL-2000; 2000CN-00117245.
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 PR 12-JUL-2000; 2000CN-00117245.
 XX
 PA (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.
 XX
 PI Chen Z, Yang L, Fang L;
 XX
 XX WFL; 2002-305615/35.
 DR
 XX
 XX
 PT Phytase gene sequence and application in yeast thereof.
 XX
 XX Disclosure; Fig 5; 48pp; Chinese.
 XX
 CC The invention relates to a coded phytase gene sequence suitable for
 CC secretion and expression in yeast and its application. It is mainly
 CC characterised by removing nucleotide sequence of +45--+146 bit from phyA
 CC total length structure gene sequence, removing Aspergillus niger signal
 CC peptide coded sequence of +1--+44 and +147--+159, connecting a part of
 CC signal peptide code sequence suitable for secretion and expression at 5',
 CC end and connecting a restriction endonuclease site at 3' end. The
 CC different carriers can be connected into said gene sequence so as to form
 CC a recombinant plasmid with different functions and after the recombinant
 CC plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
 CC yeast, finally the invented Pasteur Pichia yeast engineering bacterium
 CC (CCTCC NO:M200005) can be obtained through the screening process. By
 CC using the invention the industrial process of phytase bio-expression can
 CC be successfully implemented. The present sequence is that of a
 CC polynucleotide of the invention
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 SQ Sequence 1344 BP; 286 A; 420 C; 329 G; 309 T; 0 U; 0 Other;
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 Pred. No.: 1,82e-234 Length: 1344
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 6 Gaps: 0
 US-10-089-364-4 (1-449) x AEN85591 (1-1344)
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 Db 1 CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGCGATAGGTCGATCAGGGGTATCAA 60

QY 22 CysPheSerGlyThrSerHisLeuTrpGlyGlnTyrAlaProPheSerLeuAlaAsn 41
 Db 61 TGTCTTCTCGAGACTTCGCATCTTTGGGGTCAATACGACCGTCTTCTCTCTGCGCAAC 120
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 121 GAATCGGTCACTCTCCCTGAGGTGCCGCGGATGAGAGTCACTTCGCTCAGGTCTC 180
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerIleGlyIleValTyrSerAlaLeuIle 81
 Db 181 TCCGTCATGGAGCGGCTATCCGACCGACTCCAGGGCAAGAAATACCTCCGCTCAAT 240
 QY 82 GluGluIleGlnAsnAlaThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 241 GAGGAGATCCAGCAAGACCGGACCACTTTGAGGHAATATGCTTCTTCTGAAGACATAC 300
 QY 102 AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSer 121
 Db 301 AACTACAGCTTGGGTGCAGATGACCTGACTCTCCCTTCGAGAACAGGAGCTAGTCACTCC 360
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 361 GGCAATCAAGTTCTACCGAGCGGTACGAATCGCTCACAGGAAACATCGTTCCATTCAICCGA 420
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 421 TCTCTGGCTCCAGCGCGTGCCTCGGCAAGAAATTCATCGAGGGCTTCCAGAGC 480
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 481 ACCAAGCTGAAGGATCTCTCGTCCCGAGCCCGGCAATTCGTCGCCCAAGATCGAGTGGTC 540
 QY 182 IleSerGluAlaSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 201
 Db 541 ATTTCCGAGGCCAGCTCATCCAAACACACTCTCGACCCAGCACCTGCTGCTTCCGAA 600
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 601 GACAGCGAATGGCCGATACCGTCGAAGCCAAATTCACGCCACGTTCTGCTCCCTCAT 660
 QY 222 ArgGluArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 661 CGTCAACGCTCGAGAACGACCTGTCGCGTGTGACTCTCACAGACAGAGTGCATAC 720
 QY 242 LeuMetAspVetCysSerPheAspThrIleSerThrThrValAspThrLysLeuSer 261
 Db 721 CTATGGACATGTCTCTCTTCGACACCATCTCCACACGACCCGTCGACACCAAGCTGTC 780
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 781 CCTTCTGTGACCTGTTTCCATCCCATGAGATGAGTCAACTACGACTACCTCCAGTCTCT 840
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 841 AAAAAAGTATTACGCCCATGTGTGAGTAAACCGCTCGCGCCGACCCCGGGGGCTCGGTAC 900
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 901 GCTAACGAGCTCATCGCCCGTCTGACCCACTCGGCTGTCCACGATGACACAGTCCAC 960
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 961 CACACTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGAGCTTT 1020
 QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1021 TCGCATGACAAACGGCATCATCTCCATTCTCTTTTAGTCTGTATCAACGGGACATAAG 1080
 QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
 Db 1081 CCGCTAICTACACGACCGTGGAGAAATATACCCACAGATGAGATTCTCGTCTGCTTGG 1140

QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1141 ACGGTTCCGTTTGCTTCGGTTGTACGTCGAGATGATGCAGTGTTCAGGCGGAGGAG 1200
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 1201 CGCGTGGTCCGTTGCTTCGTTTAATGATCGCGTGTGCCGCTGCATGGGTGTCCGGTTGAT 1260
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1261 GCTTTGGGGAGATGATACCGGATAGCTTTGTAGGGGGTTGAGCTTTGCTAGATCTGGG 1320
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 1321 GGTGATGGGCGGAGTGTGTTTGTCT 1344

RESULT 4

ABN85587

ID ABN85587 standard; DNA; 1382 BP.

XX AC ABN85587;

XX AC ABN85587;

XX 17-SEP-2002 (first entry)

XX Aspergillus niger phyA related polynucleotide 1.

DE Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; ds.

XX Aspergillus niger.

XX CN133363-A.

XX 30-JAN-2002.

XX 12-JUL-2000; 2000CN-00117245.

XX 12-JUL-2000; 2000CN-00117245.

XX (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.

XX Chen Z, Yang L, Fang L;

XX WPI; 2002-305615/35.

XX Phytase gene sequence and application in yeast thereof.

XX Claim 4; Page 1 (Claims); 48pp; Chinese.

XX The invention relates to a coded phytase gene sequence suitable for secretion and expression in yeast and its application. It is mainly characterized by removing nucleotide sequence of +45-+146 bit from phyA total length structure gene sequence, removing Aspergillus niger signal peptide coded sequence of -1-+44 and +147-+159, connecting a part of signal peptide code sequence suitable for secretion and expression at 5' end and connecting a restriction endonuclease site at 3' end. The different carriers can be connected into said gene sequence so as to form a recombinant plasmid with different functions and after the recombinant plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia yeast, finally the invented Pasteur Pichia yeast engineering bacterium (CCTCC NO:M200005) can be obtained through the screening process. By using the invention the industrial process of phytase bio-expression can be successfully implemented. The present sequence is that of a claimed polynucleotide of the invention

SQ Sequence 1382 BP; 330 A; 360 C; 292 G; 400 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.9e-234	Length:	1382
Score:	2353.00	Matches:	448
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.79%	Indels:	0
DB:	6	Gaps:	0

US-10-089-364-4 (1-449) x ABN85587 (1-1382)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 Db 30 CTGGCAGTCCCAGCCTCTAGAAATCAATCTCTTGTGATCTGTGATCAGGTTATCAA 89
 QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 90 TGTCTTCTCGAGACCTTCACTTTGGGGTCAATACGCCACCAATCTTCTCTCGGCAAC 149
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 150 GAAATCTGTCACTCTCCCTGAGGTGCCAGCCGATGTAGAGTCACTTTCGCTCAGTCCCT 209
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeu 81
 Db 210 TCCAGACATGGAGCTAGATATCCAAACCGACTCCAGGGTAAAGAAATCTCCGCTCTTAT 269
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 270 GAGGAGATCCAGCAGACGCTACCACTTTGACGGAAATATGCTTCTTGAGACATAC 329
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 330 AACTACTCTTTGGGTGCAGATGACCTGACTCCATTCGGAGAACAGAGCTTGTCACTCC 389
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 390 GGTATCAAGTTCTATCCAGAGATACGAATCTTTGACAGAAACATCGTTCCATTCATCA 449
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 450 TCCCTCTGTTTCTCTAGAGTTATGCCCTCCGGTAGAAATTCATCGAGGGTTTCCAGAG 509
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 510 ACTAAGCTGAAGGATCCTAGAGCCAGCCAGCTCAATCTTCTCCAAAGATCGAGTGTCTC 569
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 570 ATTTCCGAGGCTCTTTCATCCAAACACACTCTTGACCCAGGTACTTGTACTGTCTTCGA 629
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 630 GACTCTGAATGGCCGATCTGTGAGCCCAATTTCACTGCCACTTTCTGCTCCATCCAT 689
 QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 690 AGACAAAGACTGGAGAGACGACTCTGCGGTGTACTCTTACTGACACTGAAGTTACTTAC 749
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 750 CTTATGACATGTGTCTCTCGACACTATCTCCACTTCTTACCCGTCCGACCAAGCTGTCC 809
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 810 CCATTCTGTGACCTGTTCACCATGAGATGGATCAACTACGACTACTTTCGAGTCCCTTG 869
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 870 AAAAAGTATTACGGTTCATGGTGCAGGTAAACCATTTGGGTCCAAACCCAGGGTGTCCG 929
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 930 GCTAACGAGTTGATCGGCAGACTGCCACTCTCTGTCCACGATGACACCTCTTCCAAAC 989
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 990 CACACTTGGACTCTTCTCCAGCTACCTTTCATTTGAACCTACTTGTAGCTGACTTT 1049
 QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361

Db 1050 TCTCATGACACCGTATCATCTCCATTTTGTGTTTGTAGTCTGTGTACAAACGGTACTAAG 1109
QY 362 ProLeuSerThrThrValGluAlaSerGlnThrGlnThrAspGlyPheSerSerAlaTyr 381
Db 1110 CCATTGCTTACCACTACCGTTGAGATAATATCACCCAGACAGATGGATTCTTCTGCTTGG 1169
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db 1170 ACUTGTCCTATTTGCTTCTAGATTGTACGTGAGATGATGAGTGTGAGGCTGAGCAGAG 1229
QY 402 ProLeuValArgValLeuValAlaSerArgValValProLeuHisGlyCysProValAsp 421
Db 1230 CCACCTGGTCAGAGTCTTGTGTTAATGATAGATTGTCCCACTGCATGGTGTCTGTGTAT 1289
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db 1290 GCTTTGGGTAGATGTATCCAGAGATTCTTTGTTAGAGGTTTGTCTTTTGTAGATCTGT 1349
QY 442 GlyAspTIPAlaGluCysPheAla 449
Db 1350 GGTGATGGGCTGAGTGTGTGCT 1373

RESULT 5

ID ABN85590
XX ABN85590 standard; DNA; 1389 BP.

AC ABN85590;

XX 17-SEP-2002 (first entry)

DE Aspergillus niger phyA related polynucleotide 3.

XX Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; gene; ds.

OS Aspergillus niger.

FH Key Location/Qualifiers

FT CDS 1..1347

FT /*tag= a
/product= "phyA related protein"

XX CN1333363-A.

XX 30-JAN-2002.

XX 12-JUL-2000; 2000CN-00117245.

XX 12-JUL-2000; 2000CN-00117245.

XX (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.

XX Chen Z, Yang L, Fang L;

XX WPI; 2002-305615/35.

DR P-PSDB; ABB83811.

XX Phytase gene sequence and application in yeast thereof.

XX Disclosure; Fig 4; 48pp; Chinese.

XX The invention relates to a coded phytase gene sequence suitable for
XX secretion and expression in yeast and its application. It is mainly
XX characterised by removing nucleotide sequence of +45-+146 bit from phyA
XX total length structure gene sequence, removing Aspergillus niger signal
XX peptide coded sequence of +1-+44 and +147-+159, connecting a part of
XX signal peptide code sequence suitable for secretion and expression at 5'
XX end and connecting a restriction endonuclease site at 3' end. The
XX different carriers can be connected into said gene sequence so as to form
XX a recombinant plasmid with different functions and after the recombinant
XX plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
XX yeast, finally the invented Pasteur Pichia yeast engineering bacterium
XX (CCTCC NO:IM200005) can be obtained through the screening process. By
XX using the invention the industrial process of phytase bio-expression can

CC be successfully implemented. The present sequence is that of a
CC polynucleotide of the invention

XX Sequence 1389 BP; 332 A; 362 C; 293 G; 402 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.91e-234 Length: 1389
Score: 2353.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 6 Gaps: 0

US-10-089-364-4 (1-449) x ABN85590 (1-1389)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21

Db 31 CTGGCAGTCCCGAGCTCTAGAAATCAATCTCTTTGTGATACTGTGATCAGGGTTATCAA 90

QY 22 CysPheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsn 41

Db 91 TGTTCCTCCGAGACTTCTCATCTTTGGGTCATATCGCACCACTTCTCTCTGGCAAC 150

QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61

Db 151 GAATCTGTCTATCTCCCTGAGTGCAGCGGATGTAGATCACTTTCGCTCAGGTCCTT 210

QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuLe 81

Db 211 TCCAGACATGGAGCTAGATATCCACCGACTCCAGGGTAAAGAAATATCCCGTCTTAT 270

QY 82 GluGluIleGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101

Db 271 GAGGAGTCCAGCAGAACTACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 330

QY 102 AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluValAsnSer 121

Db 331 AACTACTCTTTGGGTGCAGATGACCTGACTCCATTCGGAGAACAGAGCTTGTCAACTCC 390

QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141

Db 391 GGATCAAGTTCTTACCAGAGATACGAATCTTTGACAGAAACATCGTTCATTCATCAGA 450

QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161

Db 451 TCCTCTGGTTCCTTAGAGTTATCGCTCGGTGAGAAATTCATCAGAGGTTTCCAGAGC 510

QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181

Db 511 ACTAAGCTGAAGGATCTAGAGCCAGCCAGGTCATCTTCTCCAAAGATCGAGTGTGC 570

QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201

Db 571 ATTTCCGAGGCTTCTTCAUCCAAACACACTTTGACCCAGTACTGTACTGTCTCGAA 630

QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221

Db 631 GACTCTGAATTTGCCGATACTGTGGAAGCCAAATTCATGCCACTTTCGTCCTCCATCAT 690

QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241

Db 691 AGACAAGACTGGAGAACGACCTGTCCGGTGTGTACTTCTTACTGACACTGAAGTTACTTAC 750

QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261

Db 751 CTTATGACAGATGTGTTCTTCGACATATCTCCACTTCTACCGTCGACACCAAGCTGCC 810

QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281

Db 811 CCAATCTGTGACCTGTTCACCCCATGACGAATGGATCAACTACGACTACTTCGAGTCTCTTG 870

QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301

Db 871 AAAAGATATACGGTCATCGTCAGGTAACCCATTGGGTCCACCCAGGGGTGCGGTTAC 930
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspThrSerSerAsn 321
 Db 931 GCTACGAGCTTGATCGCCAGACTGACCCACTCTCCGTGTCACGATGACACCTCTTCCAAC 990
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 991 CACACTTTGGACTCTCTCCAGCTACCTTCCATTGCACTTACTTTGTAGCGTGACTTT 1050
 QY 342 SerHisAspAsnGlyIleLeuSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1051 TCTCAGACAAACGGTATCATCTCCATTTTGTCTTAGGCTGTACAAACGGTACTAAG 1110
 QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
 Db 1111 CCAATGCTCTACCACTACCGTTGAGATATACCCAGACAGATGGATTCTCTTGTGTTGG 1170
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1171 ACTGTTTCCATTGCTCTTAGATTGTACGTCGAGATGATCGAGTGTGAGCTGAGCAGGAG 1230
 QY 402 ProLeuValArgValLeuValAsnAspArgValProLeuHisGlyCysProValAsp 421
 Db 1231 CCACCTGGTCAGAGTCTTGTTTAAATGATAGAGTTGTCCCACTGCATGTTGTCTGTGAT 1290
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1291 GCTTTGGTAGATGATACAGAGATCTTTTGTAGAGTTTGTCTTTTCTAGATCTGTGT 1350
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 1351 GGTGATTGGGCTGAGTGTCTTGTCT 1374
 RESULT 6
 ID AAQ11175 standard; cDNA; 1404 BP.
 XX AC AAQ11175;
 XX 25-MAR-2003 (revised)
 DT 30-MAR-2000 (revised)
 DT 31-MAY-1991 (first entry)
 XX Chromosomal phytase encoding sequence.
 DE Microbial phytase; animal feed; inositol; inorganic phosphate; ss.
 KW Synthetic.
 OS
 XX Key Location/Qualifiers
 FH CDS 1..1404
 FT /*tag= a
 FT /product= "chromosomal phytase"
 FT sig_peptide 1..69
 FT /*tag= b
 XX EP420358-A.
 XX 03-APR-1991.
 XX 27-SEP-1990; 90EP-00202565.
 XX 27-SEP-1989; 89EP-00202436.
 PR 17-AUG-1990; 90EP-00202231.
 XX (KONN) GIST-BROCADES NV.
 FA (STAM) DSM NV.
 XX Van Gorcom RF, Van Hartingsveldt W, Vanparidon PA, Beenstra AE;
 PI Luiten RG, Seltén GCM;
 XX WPI; 1991-095799/14.

DR P-PSDB; AAR11333.

XX DNA encoding phytase - used for recombinant expression for prodn. of
 PT phytase for conversion of phytate to inositol and inorganic phosphate
 esp. in animal feed.

XX Disclosure; Fig 8; 61pp; English.

XX This sequence is the translation region deduced from comparisons of
 CC respective sequences of clones identified using oligonucleotide probes.
 CC The use of recombinant DNA methods for the enzyme prodn. allows the
 CC large scale prodn. of proteins and peptides having phytase activity.
 CC These are used for the conversion of phytate to inositol and inorganic
 CC phosphate and can be used in industrial processes. The phosphate content
 CC of manure thus can be decreased. See also AAQ11157-74. (Revised record
 CC issued to correct errors present in the sequence portion of the original
 CC GENESBQ entry.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 CC 25-MAR-2003 to correct PI field.)

XX SQ Sequence 1404 BP; 293 A; 436 C; 344 G; 331 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.94e-234 Length: 1404
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 2 Gaps: 0

US-10-089-364-4 (1-449) x AAQ11175 (1-1404)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 Db 58 CTGGCAGTCCCGCGCTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGGTATCAA 117
 QY 22 CysPheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 118 TCGTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGCTTCTCTCTGCGAAAC 177
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 178 GAATCGGTCACTCCCTGAGTGCGCCGCCGATGTCAGAGTCACATTCGCTCAGTCTCTC 237
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
 Db 238 TCCGCTCAAGGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATACCTCGCTCTCAT 297
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 298 GAGGAGATCCAGCAGACGCGACCCACTTTGACGGAAATATGCTTCTCTGAGACATAC 357
 QY 102 AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 358 AACTACAGCTTGGGTGCAGATGACTGACTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 417
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 418 GGCATCAAGTTCTACCGCGGTACGAATCGCTCAAGGAACATCGTTCATTCATCCGA 477
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 478 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGGTCTCAGAGC 537
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 538 ACCAAGCTGAAGGATCTCGTGGCCAGCCGCCCAATCGTCGCCCAAGATCGACGTGGTC 597
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 598 ATTTCCGAGGCCAGCTCATCCACCAACACTCTCCAGCCAGGACCTGCTGCTTCTCGAA 657
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221

Db 658 GACAGCGATTGGCCGATACCGTTCGAAGCAATTTTACCGCCACGCTTCGTCCTCCATT 717
 QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 718 CGTCAACGCTTCGAGAACGACCTGTCCGGTGTGACTCTCACGACACAGAAGTGACTAC 777
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrValAspThrLysLeuSer 261
 Db 778 CTATGGACATGTGCTTCGACACCACTCCACGACACCGTCCAGCAGCTGTCC 837
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 838 CCCTTCTGTGACCTGTTCACCCATGACGAATGGATCAACTACGACTACCTCCAGTCTCTG 897
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 898 AAAAAGTATTACGCCCATGTGTGAGGTAAACCGCTCGGCCGACCCAGGGCGTGGCTAC 957
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 958 GCTAACAGAGCTCATCGCCCTGTGACCCACTCGCCTGTCCACGATGACACCCAGTCCAAC 1017
 QY 322 HisThrIleuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 1018 CACACTTTTGACACGAGCCCGGTACCTTTCGGCTCAACTCTACTCTCTACGGCGACTTT 1077
 QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1078 TCGCATGACACCGGCATCATCTCCATCTCTTGTGCTTGTGTCGTGACACGGCACCTAAG 1137
 QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
 Db 1138 CCGCTATCTACACGACCGGTGGAGAAATATCACCCAGACAGATGGATTCTCGTCTGCTGG 1197
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1198 ACGGTTCCGTTTGTCTCGCGTTTGTACGTCGAGATGATGAGTGTACAGGGGAGCAGGAG 1257
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 1258 CCGCTGTGTCCGTGCTTGTGTTAATGATCGCGTGTGTCCTCCGTCATGGGTGTCCCGTTGAT 1317
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1318 GCTTTGGGAGATGATCCCGGATAGCTTTGTGAGGGGTTGACTTTGTAGATCTGGG 1377
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 1378 GGTGATTGGCGGAGTGTGTTTGCT 1401
 RESULT 7
 ID AA227421
 AC AA227421;
 XX
 AC AA227421;
 XX
 DT 27-AUG-2003 (revised)
 DT 07-DEC-1999 (first entry)
 XX
 DE
 XX
 XX A. ficum phytase coding sequence.
 KW Phytase; variant; enzyme; phosphorus liberation; phytase substrate;
 KW phytate level reduction; animal manure; food preparation; soy processing;
 KW inositol manufacture; ss.
 XX
 OS Aspergillus ficum.
 XX
 FN WO9949022-A1.
 XX
 PD 30-SEP-1999.
 XX
 PD 22-MAR-1999; 99WO-DK000153.
 PF
 XX

PR 23-MAR-1998; 98DK-00000407.
 PR 19-JUN-1998; 98DK-00000806.
 PR 18-SEP-1998; 98DK-00001176.
 PR 22-JAN-1999; 99DK-00000091.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Svendsen A;
 XX
 PI WPI; 1999-580444/49.
 DR F-PSDB; AAY39904.
 XX
 PT New variant phytase enzymes, used for liberating phosphorus from a
 PT phytase substrate, for reducing phytate levels in animal manure and in
 PT feed and food preparations.
 PS Disclosure; Fig 11; 141pp; English.
 XX
 CC This sequence encodes the Aspergillus ficum phytase sequence. The
 CC invention relates to variant phytase enzymes with specific amino acid
 CC substitutions for improved properties. The phytase variants can be used
 CC for liberating phosphorus from a phytase substrate. They can be used for
 CC reducing phytate levels in animal manure. They can be used in feed or
 CC food preparations. The phytase DNA can also be used to produce transgenic
 CC plants which can be used in feeds or foods. The phytase variants can also
 CC be used in soy processing and in the manufacture of inositol or
 CC derivatives. The phytase variants can have altered activities such as pH
 CC stability, temperature stability, pH profile, temperature profile,
 CC specific activity (in particular in relation to pH and temperature),
 CC substrate specificity, substrate cleavage pattern, substrate binding,
 CC position specificity, the velocity and level of release of phosphate from
 CC corn, reaction rate, phytase degradation rate and end level of released
 CC phosphate reached. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 1404 BP; 293 A; 436 C; 344 G; 331 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,94e-234 Length: 1404
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 2 Gaps: 0
 US-10-089-364-4 (1-449) x AA227421 (1-1404)
 QY 2 LeuAlaValProAlaSerArgAsnGlnSerCysAspThrValAspGlnGlyTyrGln 21
 Db 58 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGATCGATCGGGGTATCAA 117
 QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 118 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGGTTCTTCTCTCGCAAC 177
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 178 GAATCGGTCTATCTCCCTCGAGGTCCCGCGGATGCGAGTCACTTCGCTCAGGTCTCTC 237
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeulle 81
 Db 238 TCCCGTATGAGCGCGGTATCCGACGACTCCAGGGCAAGAAATATCTCGCTCTCAT 297
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 298 GAGGAGATCCAGCAGAACCGCACCTTTGACGAAAAATATGCTCTTCTGAAGACATAC 357
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 358 AACTACAGCTTGGGTGCGATGACTGACTCCCTTCGGAGAACAGGAGCTTACTTCACTCC 417
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 418 GGCATCAAGTTCTACCGAGCGGTACGATCGCTCACAGGAACATCGTTCCTCCATCCGA 477

QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 DB 478 TCCTCTGGCTCCAGCGCGTGTGCTCGGCAGAAATTCATCGAGGCTTCAGAGC 537
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 DB 538 ACCAAGCTGAGGATCCTCGTCCAGCGCGGCAATCGTCGCCAAGATCGACGTGGTC 597
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 DB 598 ATTTCGGAGCGCAGCTCAFTCCAAACACTCTCGACCCAGGACCTGCACTCTCTCGAA 657
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 DB 658 GACACGGAATGGCCGATACCTCGAGGCCAATTCACCGCCACAGTTCGTCCCTCCATT 717
 QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 DB 718 CGTCAACGCTCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAAAGTGACCTAC 777
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrValAspThrLysLeuSer 261
 DB 778 CTCATGGACATGTCTCTTCGACACCAATCTCCACGACCGCTCGACCAAGCTGTCC 837
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 DB 838 CCCTTCTGTGACCTGTTCACCATCAGCAATGATCACTACGACTACTCTCCAGTCCCTTG 897
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 DB 898 AAAAAGTATTACGGCCATGTCAGTAAACCGCTCGGCCCGACCGCGCTCGCTAC 957
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 DB 958 GCTACGAGCTCATCGCCGCTGACCACTCGCTGTCCAGTACGACCAAGTTCACAC 1017
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 DB 1018 CACACTTTGGACTCGAGCGCGGTACCTTTTCGCTCACTCTACTCTCTACGCGGACTTT 1077
 QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 DB 1078 TCGCATGACAAAGCGCATCATCTCTCTTTGCTTTAGGTCTGTACACGGGCACTAAG 1137
 QY 362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
 DB 1138 CCGCTATCTACACAGCGTGGAGAAATATCACCCAGACAGATGGATCTCGTCTGCTTGG 1197
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 DB 1198 ACGGTTCGGTTTGGTTTGGTTTGTACGTGAGATGATGCACTGTACGCGGAGCAGAG 1257
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 DB 1258 CCGTGTGTCCTGTCTTGTGTTAAATCATCGCTGTCCGCTGCATGGGTGTCGGTTCAT 1317
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 DB 1318 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGTAGCTTTGTAGATCTGGG 1377
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 DB 1378 GGTGATCGCGGAGTGTGTTGCT 1401

RESULT 8

ABN85588

ID ABN85588 standard; DNA; 1506 BP.

XX XX

AC ABN85588;

XX XX

DT 17-SEP-2002 (first entry)

XX XX

DE Aspergillus niger phyA related polynucleotide 2.
 XX Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; gene; ds.
 XX Aspergillus niger.
 XX Key Location/Qualifiers
 FT 1..1506
 FT /tag= a
 FT /product= "phyA related protein"
 FT 1..44
 FT /tag= b
 FT /number= 1
 FT 45..146
 FT /tag= c
 FT /number= 1
 FT 147..1506
 FT /tag= d
 FT /number= 2
 XX
 PN CN1333363-A.
 XX
 PD 30-JAN-2002.
 XX
 PF 12-JUL-2000; 2000CN-00117245.
 XX
 PR 12-JUL-2000; 2000CN-00117245.
 XX
 PA (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.
 XX
 PI Chen Z, Yang L, Fang L;
 XX
 WI WPI: 2002-305615/35.
 DR P-PSDB; ABE83810.
 XX
 PT Phytase gene sequence and application in yeast thereof.
 XX
 PS Disclosure; Fig 1; 48pp; Chinese.
 XX
 CC The invention relates to a coded phytase gene sequence suitable for
 CC secretion and expression in yeast and its application. It is mainly
 CC characterised by removing nucleotide sequence of +45-+146 bit from phyA
 CC total length structure gene sequence, removing Aspergillus niger signal
 CC peptide coded sequence of +1-+44 and +147-+159, connecting a part of
 CC signal peptide code sequence suitable for secretion and expression at 5'
 CC end and connecting a restriction endonuclease site at 3' end. The
 CC different carriers can be connected into said gene sequence so as to form
 CC a recombinant plasmid with different functions and after the recombinant
 CC plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
 CC yeast, finally the invented Pasteur Pichia yeast engineering bacterium
 CC (CTCC NO:M200005) can be obtained through the screening process. By
 CC using the invention the industrial process of phytase bio-expression can
 CC be successfully implemented. The present sequence is that of a
 CC polynucleotide of the invention
 XX
 SQ Sequence 1506 BP; 318 A; 465 C; 369 G; 354 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.15e-234 Length: 1506
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 6 Gaps: 0

US-10-089-364-4 (1-449) x ABN85588 (1-1506)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 DB 160 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGTATCAA 219
 QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41

Db 220 TGCCTTCGAGACTTCGCATCTTTGGGGTCAATACGCACCGCTCTCTCTCTGCGCAAC 279
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValIleu 61
 Db 280 GAATCGGTATCTCCCTCGAGTGCCTCGCGGATGCGAGATCACTTTCCTCAGGTCCTC 339
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
 Db 340 TCCCGTCTGGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATCTCCGCTCTCAT 399
 QY 82 GluGluIleGlnGlnAsnAlaThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 401
 Db 400 GAGGAGATCCAGCAGAACGCGACCACTTTGACGGAAATATGCCTTCTCTGAAGACATAC 459
 QY 102 AsnTyrSerIleuGlyAlaAspAspLeuThrProPheGlyGluGlnGluValAsnSer 121
 Db 460 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGGAACAGAGCTAGTCAACTCC 519
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 520 GGATCAAGTTCTACGACGGTACGATCGCTCAAGAGACATCGTTCATTCATCCGA 579
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 580 TCCTCTGGCTCCAGCGCGGTATCGCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGC 639
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 640 ACCAAGCTGAAGGATCTCTCGTCCCGACCGCGCAATCGTCCGCAAGATCGACGTGGTC 699
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 700 ATTTCCGAGCCAGCTCATCCACACACACTCTCGACCCAGGCACTGCATGCTTCGAA 759
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 760 GACAGCGAATGGCCGATACCGTCGAAGCCAAITTCACGCCACGTTCTGCTCCCTCCATT 819
 QY 222 ArgGlnArgIleuGluAsnAspLeuSerGlyValThrIleuThrAspThrGluValThrTyr 241
 Db 820 CGTCAACGCTTGAGAACGACCTCTCGGGTGTACTCTCACACACAGAGTGACCTAC 879
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 880 CTATGAGCATGTGCTCTCTCGACACATCTCCACGACGACCGTCCGACACCAAGCTGCC 939
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerIleu 281
 Db 940 CCTTCTGTGACCTGTTCACCCATGACGAATGGATCAACTACGACTACCTCCAGTCCCTTG 999
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProIleuGlyProThrGlnGlyValGlyTyr 301
 Db 1000 AAAAAGPATTCGCGCCATGTGCGAGTAAACCGCTCGGCCCGACCCAGGCGTCCGGTAC 1059
 QY 302 AlaAsnGluIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 1060 GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCTCTGCCAGATGACACAGTCCCAAC 1119
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 1120 CACACTTTGGACTCGAGCCGGTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1179
 QY 342 SerHisAspAsnGlyIleIleSerIlePheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1180 TCGCATGACACCGCATCATCTCTCTCTTTAGGTCTGTATACGCGGACATG 1239
 QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
 Db 1240 CCGTATCTACACGACCGTGAGATATACCCAGACAGATGATTCGTCTGCTGTTGG 1299
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1300 ACGGTTCCGTTTGCTTCGCGTTTGTAGCTCGAGATGATGCAGTGTCAAGGCGGACGAG 1359

QY 402 ProLeuValArgValValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 1360 CCGCTGGTCCGTGTCTTGGTTAATGATCGGCTGTCATGGGTGTCGGGTGAT 1419
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyIleuSerPheAlaArgSerGly 441
 Db 1420 GCTTTGGGAGATGTACCCGGGATAGCTTTGTAGGGGGTTGAGCTTTCTAGATCTGG 1479
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 1480 GGTGATTGGCGGAGTGTTTTGTCT 1503

RESULT 9

ID ADL91241 standard; DNA; 2665 BP.
 AC ADL91241;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Wild-type phytase coding sequence, SEQ ID 1.

Phytase; enzyme; foodstuff; animal feed; inositol phosphate; gene; ds.

Aspergillus niger.

WO2004024885-A2.

25-MAR-2004.

15-SEP-2003; 2003WO-US028923.

13-SEP-2002; 2002US-0410736P.

(CORR) CORNELL RES FOUND INC.

(USDA) US SEC OF AGRIC.

Lei X, Mullaney EJ, Ullah AHJ;

WPI; 2004-270029/25.

P-PSDB; ADL91242.

Novel isolated mutant phytase e.g. PhYA useful for feeding monogastric animals, improving nutritional value of foodstuffs consumed by animal, in vitro hydrolysis of phytate or improving nutritional value of foodstuffs consumed by humans.

Disclosure; SEQ ID NO 1; 215pp; English.

The present invention relates to mutant phytases (I) and their coding sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309). (I) have altered pH profiles and altered pH optima compared to a corresponding non-mutant phytase. (I) are useful for improving the nutritional value of a foodstuff which involves providing a foodstuff comprising myo-inositol hexakisphosphate, providing (I) and feeding to the animal the foodstuff in combination with (I) under conditions effective to increase the bioavailability of phosphate from phytate. (I) are also useful for feeding a monogastric animal (e.g., fowl species, porcine species, aquatic species, domestic animal chosen from canine species and a feline species, or mammalian species chosen from *Oryctolagus*, *Capra*, *Bos*, *Equus* and *Ovis* species) which involves feeding foodstuff in combination with (I), to the animal. (I) are also useful for producing specific inositol phosphate metabolites or products for nutritional and biomedical applications. The present sequence is a wild-type phytase coding sequence, which was used to produce the mutants of the invention.

Sequence 2665 BP; 633 A; 808 C; 574 G; 650 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.98e-234 Length: 2665

Score: 2353.00 Matches: 448

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 12 Gaps: 0

US-10-089-364-4 (1-449) x ADL91241 (1-2665)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 Db 842 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTGGATACGGTCGATCAGGGGTATCAA 901

QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 902 TGCCTCTCCGAGACTTCGATCTTTGGGTCAATACGCACCGCTTCTTCTCTCGGCAAC 961

QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 962 GNAATCGGTCAATCCCTCGAGTGCCCGCGGATCGAGTCACTTTCGCTCAGGTCTTC 1021

QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
 Db 1022 TCCCGTCATGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATACTCCGCTCTCAT 1081

QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 1082 GAGGAGATCCAGCAGAAACCGCACCACTTTTGACGGAATAATATGCCCTTCTCGAAGACATAC 1141

QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 1142 AACTACAGTTGGGTGAGATGACTGACTCCCTTCGGGAGAACAGAGCTAGTCAACTCC 1201

QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 1202 GGCATCAAGTTCTACAGCGGTACGAATCGCTCACAGGAACATCGTTCATTCGGA 1261

QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 1262 TCCTCTGCTCCAGCGCGGTATCGCTCCCGCAAGAAATTCATCGAGGCTTCCAGAGC 1321

QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 1322 ACCAAGCTGAGAGATCTTCGTGCCCGCCGCCAATCGTGCCCAAGATCGACGTGTC 1381

QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 1382 ATTTCCGAGGCCAGCTCATCCAAACAACACTCTCGACCCAGGACCTGCATGCTCTCGAA 1441

QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 1442 GACAGCGAATTGGCGGATACCGTCGAAGCAATTTACCGCCACCGTTCGTCCCTCCATT 1501

QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 1502 CGTCAAGCTCTGGAGACAGACTGTCCGGTGTGACTCTCACAGACACAGAAAGTGACCTAC 1561

QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 1562 CTCATGGACATGTGCTCTTCGACACCATCTCCACAGCACCGTCGACACCAAGCTGTCC 1621

QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 1622 CCCTTCTGTGACCTGTTCACCCATGACGAATGATCAACTACGACTCCAGTCCAGTCTTG 1681

QY 282 LysLysTyrTyrGlyHisGlyAlaGlnAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 1682 AAAAAGTATTACGGCCATGGGTGACGTAACCGCTCGGCCCGACCCAGCGGTCTCGCTAC 1741

QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 1742 GCTAACGAGCTCATCGCCGCTGACCCACTCGCTGTCCAGATGACACCAAGTTCACAC 1801

QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341

Db 1802 CACACTTTGGACTCGAGCCCGCTACTCTTCGCTCAACTCTCTACGGGACTTT 1861

QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361

Db 1862 TCGCATGACACACGGCATCATCTCCATTCTCTTTGCTTTAGGTCTGTACCAACGGCACTAAG 1921

QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381

Db 1922 CGCTATCTACACACCGCGTGGAGAAATATCACCGACAGATGGATCTCTGCTGCTTGG 1981

QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401

Db 1982 ACGGTTCCGTTTGTCTTCGGTTTGTACGTCGAGATGATGCAGTGTCCAGCGGAGCAGGAG 2041

QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421

Db 2042 CGCTGGTCCGCTGTCTGTTAATGATCGCTGTCCGCTGCATGGGTGTCCGGTTGAT 2101

QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441

Db 2102 GCTTTGGGGAGATGTACCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161

QY 442 GlyAspTrpAlaGluCysPheAla 449

Db 2162 GGTGATTGGGGAGTGTCTTGTCT 2185

RESULT 10

AAQ11174

ID AAQ11174 standard; DNA; 6756 BP.

XX AC AAQ11174;

DT 25-MAR-2003 (revised)

DT 31-MAY-1991 (first entry)

XX DE Sequence, from overlapping clones, encoding chromosomal phytase.

XX KW Microbial phytase; animal feeds; inositol; inorganic phosphates; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT CDS 210..1715

FT /*tag= b

FT /product= "chromosomal phytase"

FT intron 254..355

FT /*tag= a

XX EP420358-A.

XX 03-APR-1991.

XX 27-SEP-1990; 90EP-00202565.

XX 27-SEP-1989; 89EP-00202436.

XX 17-AUG-1990; 90EP-00202231.

XX (KONN) GIST-BROCADES NV.

XX (STAM) DSM NV.

XX Van Gorcom RF, Van Hartingsveldt W, Vanparidon PA, Beenstra AE;

XX Luiten RG, Selden GCM;

XX WPI; 1991-095799/14.

XX DNA encoding phytase - used for recombinant expression for prodn. of

PT phytase for conversion of phytate to inositol and inorganic phosphate

PT esp. in animal feed.

XX Disclosure; Page 32; 61pp; English.

XX This sequence is a compilation of the respective sequences of clones pAF

CC 2-3, pAF 2-6 and pAF 2-7 identified using oligonucleotide probes. The use

CC of recombinant DNA methods for the the enzyme prodn. allows the large
CC scale prodn. of proteins and peptides having phytase activity. These are
CC used for the conversion of phytate to inositol and inorganic phosphate
CC and can be used in industrial processes. The phosphate content of manure
CC thus can be decreased. See also AAQ11157-73 and AAQ11175. (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
CC field.)
XX
SQ Sequence 6756 BP; 1615 A; 1718 C; 1707 G; 1716 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1-96e-233 Length: 6756
Score: 2353.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 2 Gaps: 0

US-10-089-364-4 (1-449) x AAQ11174 (1-6756)
QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
DB 369 CTGGCAGTCCCGCCTCGAATAATCAATCCAGTTCGATACGGTCGATCAAGGGGTATCAA 428
QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
DB 429 TGGTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGCACCGTCTCTCTCTGGCAAC 488
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
DB 489 GAATCGGTATCTCCCTGAGGTGCGCGCGGATGCAGATCACTTTTCGCTCAGGTCTC 548
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerIysGlyIysIysTyrSerAlaLeuIle 81
DB 549 TCCCGTCATGAGCGCGGTATCCGACCGACTCCCAAGGGCAAGAAATACTCCGCTCTCAT 608
QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyIysTyrAlaPheLeuIysThrTyr 101
DB 609 GAGGAGATCCAGCAAGACGACCACTTTGACGGAAATATGCCCTTCCTGAACATAC 668
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
DB 669 AACTACAGCTTGGGTGCAGATGACTGACTCCCTTCGAGAAACAGGAGCTAGTCAACTCC 728
QY 122 GlyIleIysPheTyrGlnArgTyrGluSerLeuThrArgGlnIleValProPheIleArg 141
DB 729 GGCATCAAGTCTTACCAGCGGTAGCAATCGCTCCGCAAGAACATCGTTTCCATTATCCGA 789
QY 142 SerSerGlySerSerArgValIleAlaSerGlyIysIysPheIleGluGlyPheGlnSer 161
DB 789 TCCTCTGGCTCCAGCCCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGGCTCCAGAGC 848
QY 162 ThrIysLeuIysAspProArgAlaGlnProGlyGlnSerSerProIysIleAspValVal 181
DB 849 ACCAAGCTGAAGGATCCTCGTCCGACGCGCGCAATCGTCCGCCCAAGATCGAGTGCTC 908
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
DB 909 ATTTCCGAGGCCAGCTCATCCAAACACACTCTCCAGCCAGGACCTGACACTGTCTTCAA 969
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
DB 969 GACAGCGAATTGGCCGATACCGTCGAGCCAAATTCACCGCCACGTTCTGCTCCCTCCANT 1028
QY 222 ArgGlnArgLeuGluAlaAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
DB 1029 CGTCAACGCTCTGGAGACGACTCTCGGTGTGATCTCTCACAGACACAGAAAGTACCTTAC 1088
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrIysLeuSer 261
DB 1089 CTCARGGACATGTGCTCTCTCGACACCATCTCCACAGCACCGTCCGACCAAGCTGTCC 1148
QY 262 PropPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281

DB 1149 CCTTCTGTGACCTGTTCCACCATGACGAATGATCACTACGACTACCTCCAGTCTCTTG 1208
QY 282 LysIysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
DB 1209 AAAAGTATTACCGCCATGTCAGGTATACCCGCTCGGCCGACCCAGGGCGTCCGCTAC 1268
QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
DB 1269 GCTAACGAGCTCATCGCCGCTCTGACCCACTGCGCTGTCCAGATGACACCACTTCCAAC 1328
QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
DB 1329 CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCACTCTACTCTCTACGGGACTTT 1388
QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
DB 1389 TCGCATGACAAACGGCATCATCTCCATCTCTTTGCTTTAGTCTGTACACGGCAGCTAAG 1448
QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
DB 1449 CCGCTATCTACCAACGACCGGTGGAGATATCACCACAGACAGATGGATTCTCGTCTGTGG 1508
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
DB 1509 ACGGTTCCGTTTCTCGGCTTTGTACGTGAGATGATGCAGTGTCCAGGCGGAGCAGGAG 1568
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
DB 1569 CCGCTGGTCCGTCGTCTGTGGTTAATGATCCGCTGTGTCCGCTGATGGGTTCGGTTGAT 1628
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
DB 1629 GCTTTGGGAGAGTACCCCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1688
QY 442 GlyAspTrpAlaGluCysPheAla 449
DB 1689 GGTGATTGGCGGAGTGTGTTGCT 1712

RESULT 11
AAT65137
ID AAT65137 standard; cDNA; 6756 BP.
XX AC AAT65137;
XX DT 17-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 21-AUG-1997 (first entry)
XX DE Aspergillus ficuum phytase genomic DNA.
XX KW Phytase; phytate; inositol; animal feed; ss.
XX OS Aspergillus ficuum; NRRL 3135.
XX PH Key Location/Qualifiers
XX FT primer_bind /*tag= d (210..231)
XX FT /*note= "oligonucleotide 1"
XX FT exon 211..253
XX FT /*tag= a
XX FT intron 254..355
XX FT /*tag= b
XX FT exon 356..1715
XX FT /*tag= c
XX FT primer_bind complement(845..865)
XX FT /*tag= f
XX FT primer_bind /*note= "oligonucleotide 3"
XX FT 1109..1129
XX FT /*tag= e
XX FT primer_bind /*note= "oligonucleotide 2"
XX FT 1867..1890
XX FT /*tag= g

/note= "oligonucleotide 4"

FT XX EP779037-AL.
 PN XX
 XX XX
 PD 18-JUN-1997.
 XX XX
 PF 27-SEP-1990; 96EP-00202943.
 XX XX
 PR 27-SEP-1989; 89EP-00202436.
 PR 17-AUG-1990; 90EP-00202231.
 PR 27-SEP-1990; 90EP-00202565.
 XX XX
 PA (KONN) GIST-BROCADES NV.
 PA (STAM) DSM NV.
 XX XX
 PI Van Paridon PA, Veenstra AE, Luiten RGM, Selten GCM;
 PI Van Gorcom RFM, Van Hartingsveldt W;
 XX XX
 DR WPI; 1997-312513/29.
 DR P-PSDB; AAW15124.
 XX XX
 PT Fungal phytase - releases inorganic phosphate from myoinositol phosphate,
 PT useful to prepare animal feed and reduce phytate levels in manure.
 XX XX
 PS Example 8; Fig 6; 6ipp; English.
 XX XX
 CC Genomic DNA (AAT65137) comprises the phytase gene locus of *Aspergillus*
 CC ficum and includes a coding sequence, interrupted by a single intron,
 CC for the 467-amino acid enzyme (AAW15124). The DNA sequence was deduced
 CC from clones pAF 2-3, pAF 2-6 and pAF 2-7, which were identified in
 CC genomic DNA using probes (see also AAT65138-40) based on CNBr peptides
 CC (AAW15128-29) of the phytase. PCR primers (AAT65144-47) based on gene
 CC sequences were used to amplify a full-length cDNA clone (AAT65136) for
 CC the phytase. Characterisation of the phytase gene will allow large-scale
 CC prodn. of phytase in transformed host cells for use e.g. in the food and
 CC animal feed industries, and for reducing phytate levels in manure.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
 CC on 25-MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to
 CC standardise OS field)
 XX XX
 SQ Sequence 6756 BP; 1615 A; 1714 C; 1712 G; 1715 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.96e-233 Length: 6756
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 Gaps: 0

US-10-089-364-4 (1-449) x AAT65137 (1-6756)

Qy 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAlaGlnGlyTyrGln 21
 Db 369 CTGGCAGTCCCGCGCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAA 428
 Qy 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 429 TGCCTCTCCGAGACTTCGCATCTTTGGGGTCAATACGCACCGCGTCTCTCTCGGCAAC 488
 Qy 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 489 GAATCGGTCACTCCCTGAGGTGCCCGCGATGACAGTCACTTCCTGCTCAGGTCTC 548
 Qy 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
 Db 549 TCCCGTCATGAGCGCGGTATCCGACCGACTCCCAAGGGCAAGAAATATCTCGCTCTCAT 608
 Qy 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 609 GAGGAGATCCAGCAGACCGACCCACTTTTACGCGAAATATGCTTCTTCTTGAAGACATAC 668

Qy 102 AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 669 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGAGCTAGTCACTCC 728
 Qy 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 729 GGCATCAAGTTCTACACGGGTACGAATCGCTCACAGGAACATCGTTCCATTCTCCGA 788
 Qy 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 789 TCCCTCTGGCTCCAGCCGCTGATCCCTCCGGCAAGAAATTCATCGGGGTCTCAGAGC 848
 Qy 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 849 ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGGCCATCGTCCGCCAAGATCGACGTGTC 908
 Qy 182 IleSerGluAlaSerSerSerAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 909 ATTTCCGAGGCGAGCTCATCCAAACACTCTCGACCCAGGCACCTGCTGCTCTTCGAA 968
 Qy 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 969 GACAGCGAATTGGCGGATACCGTCGAAGCCAATTTCAACGCCACGTTCTGCTCCCTCCAT 1028
 Qy 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 1029 CGTCAACGCTCGAGAGAGACCTGTCCGGTGTGACTCTCACAGACACAGAGTACCTTAC 1088
 Qy 242 LeuMetAspMetCysSerPheAspThrIleSerThrValAspThrLysLeuSer 261
 Db 1089 CTCATGAGATGTGCTCTCCACACCATCTCCACCCAGCACCGTCGACCAAGCTGTCC 1148
 Qy 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 1149 CCCTTCTGTGACCTGTTTCAACCATGAGAAATGGATCACTACGACTACTCTCCAGTCTTG 1208
 Qy 282 LysLysTyrTyrGlyHisGlyValAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 1209 AAAAAGTATTACGGCCATGTTGCGAGGTAAACCGCTCGGCCCGACCCAGGGGGTGGCTTAC 1268
 Qy 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 1269 GCTAAACAGAGCTCATCGCCGCTCGACCATCGCTGTCCACGATGACACAGTTCCCAAC 1328
 Qy 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 1329 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1388
 Qy 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1389 TCGCATGACACACGCATCACTCCATTTCTTTGCTTTAGGTCTGTACAAGGACCTAAG 1448
 Qy 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
 Db 1449 CCGCTACTACACGACCGGTGGAGAAATATACCCAGACAGATGATTCGTCTGCTGTGG 1508
 Qy 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1509 ACGGTTCCGTTGCTTCGCTTTGTACGTGAGATGATGACAGTGTGAGGGGAGACGAG 1568
 Qy 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 1569 CCGCTGTGCTGCTTGTGTTATGATCGGGTGTCCGCTGCGATGGGTGTCCGGTGTAT 1628
 Qy 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1629 GCTTTGGGAGATGTATCCCGGATAGCTTTGTGAGGGGGTTGACTTTGTCTAGATCTGG 1688
 Qy 442 GlyAspTrpAlaGluCysPheAla 449
 Db 1689 GGTGATTGGCGGAGTGTGTTTGTCT 1712

RESULT 12

Db 1449 CCCTATCTACCGACCGTGGAGATATACCCAGACAGATGATCTCGTCTGCTGG 1508
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1509 ACGTTCCGTTTCTTCCGTTTGTAGTTCAGTTCAGATGATGAGTGTGAGCGGAGCAGGAG 1568
 QY 402 ProLeuValArgValLeuValAenAspArgValProLeuHisGlyCysProValAsp 421
 Db 1569 CCGCTGGTCCGTGTCTTGTATGATCGCTTGTCCCGTGTCCGCTGCTCGGTTGAT 1628
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1629 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTGTGAGCTTTGCTAGATCTGG 1688
 QY 442 GlyAspTirAlaGluCysPheAla 449
 Db 1689 GGTGATGGCGGAGTGTGTGCT 1712
 RESULT 13
 ABN85592
 ID ABN85592 standard; DNA; 1344 BP.
 XX
 AC ABN85592;
 XX
 DT 17-SEP-2002 (first entry)
 XX
 DE Aspergillus niger phyA related polynucleotide 5.
 XX
 KW Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; gene; ds.
 XX
 OS Aspergillus niger.
 XX
 XN CN133363-A.
 XX
 PD 30-JAN-2002.
 XX
 PF 12-JUL-2000; 2000CN-00117245.
 XX
 PR 12-JUL-2000; 2000CN-00117245.
 XX
 PA (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.
 XX
 PI Chen Z, Yang L, Fang L;
 XX
 DR WPI; 2002-305615/35.
 XX
 PT Phytase gene sequence and application in yeast thereof.
 XX
 PS Disclosure; Fig 5; 48pp; Chinese.
 XX
 CC The invention relates to a coded phytase gene sequence suitable for
 CC secretion and expression in yeast and its application. It is mainly
 CC characterised by removing nucleotide sequence of +45-+146 bit from phyA
 CC total length structure gene sequence, removing Aspergillus niger signal
 CC peptide coded sequence of +1-44 and +147-+159, connecting a part of
 CC signal peptide code sequence suitable for secretion and expression at
 CC end and connecting a restriction endonuclease site at 3' end. The
 CC different carriers can be connected into said gene sequence so as to form
 CC a recombinant plasmid with different functions and after the recombinant
 CC plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
 CC yeast, finally the invented Pasteur Pichia yeast engineering bacterium
 CC (CCTCC NO:M200005) can be obtained through the screening process. By
 CC using the invention the industrial process of phytase bio-expression can
 CC be successfully implemented. The present sequence is that of a
 CC polynucleotide of the invention
 XX
 SQ Sequence 1344 BP; 316 A; 355 C; 280 G; 393 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3 73e-234 Length: 1344
 Score: 2350.00 Matches: 447
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.78% Mismatches: 0

Query Match: 99.66% Indels: 0
 DB: 6 Gaps: 0
 US-10-089-364-4 (1-449) x ABN85592 (1-1344)
 QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 Db 1 CTGGCAGTCCGAGCCTCTAGAAATCAATCTCTTGTGATACCTGATCAGGGTTATCAA 60
 QY 22 CysPheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 61 TGTTCCTCCGAGACTTCTCATCTTGGGTCAATACGACCATTTCTTCTCTCTGGCAAC 120
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 121 GAAATCTGTCTATCTCCCTCAGGTGCCGCGATGTAGAGTCACATTCGCTCAGCTCCTT 180
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
 Db 181 TCCAGACATGGAGCTAGATATCCACCGACTCCAGGGTAAGAAATATCTCCGCTCTTATT 240
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 241 GAGGAGATCCAGCAGAACGCTACCACTTTCAGCGAAATATGCTTCTCTGAAGACATAC 300
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGlyGlnGluLeuValAsnSer 121
 Db 301 AACTACTCTTTGGGTGCAGATGACCTGACTCCATTCGGAGAACAGAGGCTTGTCACTCC 360
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 361 GGTATCAAGTTCTACAGAGATACGAATCTTTGACAAGAAACATGTTCCATTCATCAGA 420
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 421 TCCTCTGGTTCCTTAGAGTTATCGCTCCGGTAAGAAATTCATCGAGGTTTCCAGAGC 480
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 481 ACTAAGCTGAAGGATCCTAGAGCCAGCCAGCGTCAATCTCTCCAAAGATCCAGCTTGT 540
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 541 ATTTCCGAGGCTCTTTCATCCAAACACACTCTTGACCCAGGTACTTGTACTGTCTTCGAA 600
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 601 GACTCTGAATTGGCGGATACGTGCGAAGCCAATTTCACTGCCACTTTCGTCCCATCCATT 660
 QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 661 AGACAAAGACTGGAGAGACGACTGTCCGGTGTACTCTTACTTGACACTGAAGTTACTTAC 720
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 721 CTTAAGACATGTGTCTCTTCGACACTATCTCCACTTACCGTCGACACCAAGCTGTCC 780
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 781 CCATTTCTGTGACCTGTTTCAACCATGACGAATGGATCAACTACGACTACTTTCAGTCCCTT 840
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 841 AAAAAGTATTACGGTTCATGGTGCAGGTAACCATTTGGGTCCAAACCCAGGGTGTGGTTAC 900
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 901 GCTAACGAGTTGATCGCCAGACTGACCCACTCTCTCTGTCCACGATGACACTCTTCCAAC 960
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 961 CACACTTTGGACTCTTCTCCAGCTACCTTTCCATTGAACCTACTATTGTGACGTGACTTTT 1020

Db 1622 CCCTCTGTGACCTGTTACCCATGACGAATGGATCAACTACGACTACCTCCAGTCTCTTG 1681

QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301

Db 1682 AGAAGATTACGGCAUGTTCAGGTAACCGCTCGGCCGCCAGCCAGGGCGTTCGGCTAC 1741

QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerAsn 321

Db 1742 GCTAAACGAGCTCATGCCCGTCTGACCCACTCGCTGTCCAGATGACACACAGTCCCAAC 1801

QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrIeuTyrlaasphe 341

Db 1802 CACATTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1861

QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361

Db 1862 TCGCATGACACGGCATCATCTCCATCTCTTTGCTTTAGTCTGTACACGGCACTAAG 1921

QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381

Db 1922 CCGCTATCTACACACCGTGGAGAATATCACCCAGACAGATGGATTCTCGTCTGCTTG 1981

QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnlu 401

Db 1982 ACGGTTCCGTTTTCCTTCGCTTTGTACGTCGAGATGATGCAATGTCAGCGGAGGAG 2041

QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421

Db 2042 CCGCTGGTCCGTTCTTGGTTAAATGATCGCTTGTCCGCTGCAATGGGTTCGGTTGAT 2101

QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441

Db 2102 GCTTTGGGGAGATGATACCGGGGATAGCTTTGTAGGGGGTTGAGCTTTGCTAGATCTGG 2161

QY 442 GlyAspTrpAlaGluCysPheAla 449

Db 2162 GGTGATGGCGGAGTGTGTTGCT 2185

RESULT 15

ID ADL91261 standard; DNA; 2665 BP.

XX ADL91261;

AC ADL91261;

XX 17-JUN-2004 (first entry)

DT Mutant phytase, E228Q, coding sequence, SEQ ID 21.

XX Mutant; mutein; phytase; enzyme; foodstuff; animal feed;

XX inositol phosphate; gene; ds.

OS *Aspergillus niger*.

OS Synthetic.

XX WO2004024885-A2.

FN 25-MAR-2004.

XX 15-SEP-2003; 2003WO-US028923.

PF 13-SEP-2002; 2002US-0410736P.

XX (CORR) CORNELL RES FOUND INC.

XX (USDA) US SEC OF AGRIC.

XX Lei X, Mullaney EJ, Ullah AHJ;

XX WPI; 2004-270029/25.

DR P-PSDB; ADL91262.

XX Novel isolated mutant phytase e.g. Phya useful for feeding monogastric

PT animals, improving nutritional value of foodstuffs consumed by animal, in

ET vitro hydrolysis of phytate or improving nutritional value of foodstuffs

PT consumed by humans.

XX Claim 5; SEQ ID NO 21; 215pp; English.

XX The present invention relates to mutant phytases (I) and their coding sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309). (I) have altered pH profiles and altered pH optima compared to a corresponding non-mutant phytase. (I) are useful for improving the nutritional value of a foodstuff which involves providing a foodstuff comprising myo-inositol hexakisphosphate, providing (I) and feeding to the animal the foodstuff in combination with (I) under conditions effective to increase the bioavailability of phosphate from phytate. (I) are also useful for feeding a monogastric animal (e.g., fowl species, porcine species, aquatic species, domestic animal chosen from canine, Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding foodstuff in combination with (I), to the animal. (I) are also useful for producing specific inositol phosphate metabolites or products for nutritional and biomedical applications. The present sequence is the coding sequence for one such mutant phytase.

XX Sequence 2665 BP; 633 A; 809 C; 573 G; 650 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.02e-233 Length: 2665

Score: 2350.00 Matches: 447

Percent Similarity: 100.00% Conservatives: 1

Best Local Similarity: 99.78% Mismatches: 0

Query Match: 99.66% Indels: 0

DB: 12 Gaps: 0

US-10-089-364-4 (1-449) x ADL91261 (1-2665)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21

Db 842 CTGGCAGTCCCGCGCTCGAGAAATCAATCCAGTTCCGATACGGTGCATCGAGGTATCAA 901

QY 22 CysPheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaSer 41

Db 902 TGCTTCTCCGAGACTTCGATCTTTGGGTCAATACGACCGCTTCTCTCTGCGCAAC 961

QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61

Db 962 GAATCGGTCACTCCCTGAGTGCCTGGATGCGAGTCACTTTCGCTCAGGTCTCTC 1021

QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeulle 81

Db 1022 TCCCGTCATGGAGCGCGGTATCCGACCGACTCCAAAGGGCAAGAAATACCTCGCTCTCAT 1081

QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101

Db 1082 GAGGAGATCCAGCAGAACGCGACCCCTTTGACGGAAATATGCCCTTCTCGAAGACATAC 1141

QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121

Db 1142 AACTACAGTTGGGTGCGAGATGACCTGACTCCCTTCGGAGAACAGAGTAGTCACTCC 1201

QY 122 GlyTleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141

Db 1202 GGCAATCAAGTTCTACACGCGGTACGAATCGCTCAAGGAACATCGTTCCATTTCATCGA 1261

QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161

Db 1262 TCCCTCGCTCCAGCCCGGTGATCGCTCCGGAGAAATTCATCGAGGGCTTCCAGAGC 1321

QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181

Db 1322 ACCAAGCTGAAGGATCTCTGTCGCCACCGGCCAATCGTCGCCCAAGATCGAGTGGTC 1381

QY 182 IleSerGluAlaSerSerSerAsnAsnThrIeuAspProGlyThrCysThrValPheGlu 201

Db 1382 ATTTCCGAGGCCAGCTCATCCAAACACACTCTCGACCCGAGCACCTGCTCTCTCGAA 1441

```
Qy 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db |||||
Db 1442 GACAGCGAATGGCCGATACCGTCCAGCAATTTCCCGCCACGTTCTGCCCTCCATT 1501
Qy 222 ArgGlnArgGluLeuAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db |||||
Db 1502 CGTCAACGTCGTGAGAACGACCTGTCGGGTGTGACTCTCACAGACACAGAGTGACCTAC 1561
Qy 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrIleSerLeuSer 261
Db |||||
Db 1562 CTCATGGACATGTGCTCCTTCGACACCATCTCCACCAGCACCGTCGACACCAAGCTGTCC 1621
Qy 262 ProPheCysAspLeuPheThrHisAspGluTyrIleAsnTyrAspTyrLeuGlnSerLeu 281
Db |||||
Db 1622 CCCCTTCGTGACCTGTTACCCATGAGATGGATCACTACGACTACCTCCAGTCTCTTG 1681
Qy 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db |||||
Db 1682 AAAAAGTATTACGGCCATGGTGCAGGTAAACCGCTCGGCCGACCCAGGGCGTCCGGCTAC 1741
Qy 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db |||||
Db 1742 GCTAACGAGCTCATCCCGCTCTGACCCACTCGCTCTGCCATGACACCAAGTCCAAAC 1801
Qy 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db |||||
Db 1802 CACACTTTGGACTCGAGCCCGGCTACTTTCCGCTCACTCTACTCTCTACGGGACTTT 1861
Qy 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db |||||
Db 1862 TCGCATGACACACGGCATCATCTCCATCTCTTTGCTTTAGGTCTGTACAAACGGCCTAAG 1921
Qy 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
Db |||||
Db 1922 CCGCTATCTACACGACCGGTGGAGATATACCCAGACAGATGGATTCTCGTCTGCTGG 1981
Qy 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db |||||
Db 1982 ACGTTCGGTTTGGTTCGCGTTTGTAGCTCGAGATGATGATGTCAGTGTCAAGCGGAGCAGGAG 2041
Qy 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db |||||
Db 2042 CCGCTGTCGCTGCTTTGTTAATGATCGGCTTGTCCCGCTGCATGGGTGTCCGGTTGAT 2101
Qy 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db |||||
Db 2102 GCTTTGGGGAGATGTACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 2161
Qy 442 GlyAspTrpAlaGluCysPheAla 449
Db |||||
Db 2162 GGTGATTGGCGGAGTGTGTTTGCT 2185
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Search completed: October 24, 2004, 13:39:01
Job time : 862 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 15:51:50 ; Search time 806 Seconds
(without alignments)

2854.393 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MLAVPASRNQSSCDTVDQY.....SFVGLSFARSGDWAECFA 449

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Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 6814466

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10089364 -CGN 1.1 912 @runat_22102004_184729_16389
-NCPU=6 -ICPU=3 -NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2353	99.8	2665	17	US-10-662-914-1
3	2353	99.8	6756	15	US-10-079-709-31
4	2350	99.7	2665	17	US-10-662-914-21
5	2350	99.7	2665	17	US-10-662-914-27
6	2349	99.6	2665	17	US-10-662-914-7
7	2349	99.6	2665	17	US-10-662-914-17
8	2349	99.6	2665	17	US-10-662-914-19
9	2349	99.6	2665	17	US-10-662-914-23
10	2349	99.6	2665	17	US-10-662-914-33
11	2347	99.5	2665	17	US-10-662-914-5
12	2347	99.5	2665	17	US-10-662-914-15
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14	2347	99.5	2665	17	US-10-662-914-31
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21	2343	99.4	2665	17	US-10-662-914-43
22	2342	99.3	2665	17	US-10-662-914-68
23	2341	99.3	2665	17	US-10-662-914-49
24	2341	99.3	2665	17	US-10-662-914-51
25	2340	99.2	2665	17	US-10-662-914-53
26	2339	99.2	2665	17	US-10-662-914-45
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28	2327	98.7	2665	17	US-10-662-914-55
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33	1820	77.2	1426	15	US-10-442-538-140
34	1818	77.1	1426	15	US-10-421-112-3
35	1818	77.1	1426	15	US-10-442-538-117
36	1806	76.6	1404	15	US-10-442-538-164
37	1618.5	68.6	1455	17	US-10-662-914-9
38	1617.5	68.6	1425	14	US-10-213-990-23
39	1617.5	68.6	1455	14	US-10-213-990-22
40	1617.5	68.6	1455	17	US-10-662-914-3
41	1617.5	68.6	1571	14	US-10-062-948-10
42	1617.5	68.6	1571	17	US-10-776-104-19
43	1610.5	68.3	1398	10	US-09-803-454-19
44	1610.5	68.3	1404	15	US-10-442-538-166
45	1534	65.1	1443	15	US-10-369-493-36558

ALIGNMENTS

RESULT 1
US-10-079-709-33
; Sequence 33, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorpom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/079,709
  FILING DATE: 02-FEB-2002
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/233,510
    FILING DATE: 20-JAN-1999
    APPLICATION NUMBER: 07/688,578
    FILING DATE: 24-MAY-1991
    ATTORNEY/AGENT INFORMATION:
      NAME: Murashige, Kate H.
      REGISTRATION NUMBER: 29,959
      REFERENCE/DOCKET NUMBER: 24615-20026.00
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415-327-7250
    TELEFAX: 415-327-2351
  INFORMATION FOR SEQ ID NO: 33:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1404 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA to mRNA
      HYPOTHETICAL: NO
      ANTI-SENSE: NO
      ORIGINAL SOURCE:
        ORGANISM: Aspergillus ficum (Aspergillus niger)
        STRAIN: NRRL 3135
        US-10-079-709-33

Alignment Scores:
Pred. No.: 1,57e-272 Length: 1404
Score: 2353.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 15 Gaps: 0

US-10-089-364-4 (1-449) x US-10-079-709-33 (1-1404)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAlaGlnGlyTyrGln 21
DB 58 CTGCAGTCCCGCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGTATCAA 117
QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
DB 118 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGCTTCTTCTCTCGCAAAC 177
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
DB 178 GAATCGGTCATCTCCCTGAGGTGCCCGCGATGCGAGTCACTTCGCTCAGTCTCTC 237
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
DB 238 TCCCGTCATGAGCGCGGTATCCGACCGACTCCAAAGGGCAAGAAATATCCGCTCTCAT 297
QY 82 GluGluIleGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuIleThrTyr 101
DB 298 GAGGAGATCCAGCAGAAACCGACCACTTTACCGAAATATGCTTCTTGAAGACATAC 357
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
DB 358 AACTACAGCTTGGGTGCGATGACCTGACTCCCTTCGAGACACAGAGCTAGTCACTCC 417
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
DB 418 GGCATCAAGTTCTACAGCGGTACGAATCGCTCACAAAGAAACATCGTTCCATTATCCGA 477

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QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
DB 478 TCCTCTGGCTCCAGCCGGTGATCGCTCCGCGCAAGAAATTCATCAGGGCTTCAGAGC 537
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
DB 538 ACCAAGCTGAAGGATCCTCGTCCAGCCCGGCAATCGTCGCCCAAGATCGACGTGGTC 597
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
DB 598 ATTTCGAGGCGAGCTCATCCAAACACTCTCGACCCAGGACCTGCACTGCTTCGAA 657
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
DB 658 GACAGCGAATTGGCCGATACCGTCGTAAGCAATTTCAAGCCCACTTCGTCCTCCATT 717
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
DB 718 CGTCAACGCTTGAGAACGACCTTCGCGGTGACTCTCACAGACACAGAAAGTGACTAC 777
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
DB 778 CTCATGACATGTGCTTCCTTCGACACATCTCCACGACACCGTCGACACCAAGCTGCC 837
QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
DB 838 CCCTTCTGTGACTGTTCACCCATGACGAATGATCAACTACGACTACCTCCAGTCTCTTG 897
QY 282 LysLysTyrTrpGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
DB 898 AAAAAGTATTACGGCCATGGTGCAGGTAAACCCGCTCGGCCGACCCAGGGCGCTCGCTAC 957
QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
DB 958 GCTAACGAGCTCATCGCCCGCTCTGACCCACTCGCCTGTCCACGATGACACCAAGTCCAAC 1017
QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
DB 1018 CACACTTTGGACTCGAGCCGGGTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1077
QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
DB 1078 TCGCATGACAAACGGCATCATCTCCATTCTTTGCTTTAGGTCGTGTACAACGGCCTAAG 1137
QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
DB 1138 CCGCTATCTACCGACCGCTGGAGAAATATCAACGACAGACAGATGGATTCCTGCTGCTGG 1197
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
DB 1198 ACGGTTCCGTTTGGTTCGCGTTTGTACGTCGAGATGATCGAGTGTCAAGCGCGAGAG 1257
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
DB 1258 CCGCTGGTCCGCTGCTTGGTTAATGATCGCGCTGTCGCGCTGATGGGTGCTCCGCTGAT 1317
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
DB 1318 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGTAGATCTGGG 1377
QY 442 GlyAspTrpAlaGluCysPheAla 449
DB 1378 GGTGATTGGCGGAGTGTGTTTGCT 1401

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RESULT 2

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US-10-662-914-1
; Sequence 1, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.

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; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES

; FILE REFERENCE: 19603/4261

; CURRENT APPLICATION NUMBER: US/10/662,914

; PRIOR FILING DATE: 2003-09-15

; PRIOR APPLICATION NUMBER: 60/410,736

; PRIOR FILING DATE: 2002-09-13

; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2665

; TYPE: DNA

; ORGANISM: Aspergillus niger

; US-10-662-914-1

Alignment Scores:

Pred. No.: 4,466-272 Length: 2665
Score: 2353.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-1 (1-2665)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
DB 842 CTGGCAGTCCCGCGCTCGAGAATCAATCCAGTTCCGATACGGTCAGGGGTATCAA 901
QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
DB 902 TGCCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGACCGTTCTTCTCTGGCAAC 961
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
DB 962 GAATCGGTCACTCCCTGAGTGGCCCGCGATCGAGTCACTTTGCTCAGTCTCTC 1021
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
DB 1022 TCCCGTCAATGAGCGCGGTATCCGACCGACTCCAAAGGGCAAGAAATATCTCCGCTCTCAT 1081
QY 82 GluGluIleGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheIleLysThrTyr 101
DB 1082 GAGGAGATCCAGCAGAACCGCACCACTTTGACGGAATAATATGCTTCTCGAAGACATAC 1141
QY 102 AsnTyrSerLeuGlyValaAspAspLeuThrProPheGlyGluGlnGluValAsnSer 121
DB 1142 AACTACAGCTTGGGTGAGATGACTGCTCCCTTCGAGACAGAGACTAGTCAACTCC 1201
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
DB 1202 GGCATCAAGTTCTACAGCGGTACGAAATCGCTCAAGGAACATCGTTCCATTCATCCGA 1261
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
DB 1262 TCCCTGTGCTCCAGCGGTGATCGCTCCGCGAAGAAATTCATCGAGGGCTTCAGAGC 1321
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
DB 1322 ACCAAGCTGAAGATCTCGTCCCGAGCCCGGCAATCGTCCGCAAGATCGAGTGGTC 1381
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
DB 1382 ATTTCCGAGGCGAGCTCATCCAAACAACTCTCGACCCAGGCACTGCACTGTCTTCGAA 1441
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
DB 1442 GACAGCGAATTTGGCGGATACCGTGAAGCCAAATTCACCGCACGTTCTCGTCCCTCCATT 1501
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
DB 1502 CGTCAAGCTCGGAGACGACCTGCTCCGGTGTGACTCTCACAGACACAGAAAGTGACCTAC 1561
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrValAspThrLysLeuSer 261

DB 1562 CTCATGGAGCATGTGCTCTCTTCGACACCATCTCCACAGACCGTCCGACACCAAGCTGTCC 1621
QY 262 ProPheCysAspLeuPheThrHisAspGluThrPheAsnTyrAspTyrLeuGlnSerLeu 281
DB 1622 CCGCTTCTGTGACCTGTTACCCCATGACGAATGGATCAACTAGCACTACCTCCAGTCTCTTG 1681
QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
DB 1682 AAAAAGTATTACGGCCATGGTGCAGTAACCCGCTCGGCCCGACCCAGGGCGCTCGGCTAC 1741
QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
DB 1742 GCTAACGAGCTCATCGCCGCTCTGACCCACTGCTGCTCCAGATGACACCAAGTCCAAAC 1801
QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
DB 1802 CACACTTTGGACTCGAGCCCGGCTACCTTTTCGGTCAACTCTACTCTCTACCGGACTTT 1861
QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
DB 1862 TCGCATGACACGGCATCATCTCCATTTCTTTGCTTTAGGTCTGTACACCGGCACTAAG 1921
QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
DB 1922 CGGCTATCTACCAACGACCGTGGAGAAATATCACCCAGACAGATGGATTCTCGTCTGTTGG 1981
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
DB 1982 ACGGTTCCGCTTTCGCTTCGCTTTGTACGTCAGAGATGATGATGTCAGCGGAGCAGGAG 2041
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
DB 2042 CGCTGTGTCGCTGCTTGTGTTAATGATCGGTTGTCCCGCTGCATGGGTGTCGGGTGAT 2101
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
DB 2102 GCTTTGGGGAGATGTACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 2161
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RESULT 3

US-10-079-709-31

; Sequence 31, Application US/10079709

; Publication No. US20030119163A1

; GENERAL INFORMATION:

; APPLICANT: Robert F.M. Van Gorcom

; APPLICANT: Willem Van Hartingsveldt

; APPLICANT: Petrus A. Van Paridon

; APPLICANT: Annemarie B. Veenstra

; APPLICANT: Rudolf G.M. Luttin

; APPLICANT: Gerardus Selten

; TITLE OF INVENTION: Cloning and Expression of Microbial

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Morrison & Foerster

; STREET: 545 Middlefield Road, Suite 200

; CITY: Menlo Park

; STATE: California

; COUNTRY: USA

; ZIP: 94025-3471

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; SOFTWARE:

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/079,709

; FILING DATE: 02-FEB-2002

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CLASSIFICATION:
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/233,510
  FILING DATE: 20-JAN-1999
  APPLICATION NUMBER: 07/688,578
  FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
  NAME: Murashige, Kate H.
  REGISTRATION NUMBER: 29,959
  REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 415-327-7250
  TELEFAX: 415-327-2951
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
  LENGTH: 6756 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
  ORGANISM: Aspergillus ficuum (Aspergillus niger)
  STRAIN: NRRL 3135
IMMEDIATE SOURCE:
  LIBRARY: lambda AF
  CLONE: pAF2-3, pAF2-6, pAF2-7
FEATURE:
  NAME/KEY: exon
  LOCATION: 210..253
FEATURE:
  NAME/KEY: intron
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FEATURE:
  NAME/KEY: exon
  LOCATION: 356..1715
FEATURE:
  NAME/KEY: CDS
  LOCATION: join(210..253, 356..1715)
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OTHER INFORMATION: /product= "Phytase"
FEATURE:
  NAME/KEY: sig_peptide
  LOCATION: 210..380
FEATURE:
  NAME/KEY: mat_peptide
  LOCATION: 381..1712
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "inositol phosphate
OTHER INFORMATION: phosphatase"
OTHER INFORMATION: /product= "Phytase"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-10-079-709-31

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Alignment Scores:
Pred. No.: 2,04e-271 Length: 6756
Score: 2353.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 15 Gaps: 0

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US-10-089-364-4 (1-449) x US-10-079-709-31 (1-6756)

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42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
489 GAATCGGTCATCTCCCTGAGGTGCGCGCGGATGCAGAGTCACTTCCTCAGGTCTC 548
62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaIle 81
549 TCCCGTCATGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATACCTCCGCTCT 608
82 GluGluIleGlnAlaSerAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThr 101
609 GAGGAGATCCAGAGAACCGGACCACTTTGACGGAAATATAGCTTCTCCTGAACAT 668
102 AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGlnGlnGluLeuValAsnSer 121
669 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGAGAACAGGAGGTAGTCA 728
122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIle 141
729 GGCATCAAGTTCTACCAAGCGGTACGAATCGCTCACAAGGAACATCGTTCATTC 788
142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGln 161
789 TCCTCTGGCTCCAGCCCGGTGATCGCTCGGCAAGAAATTCATCGAGGGCTTCC 848
162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspVal 181
849 ACCAAGCTGAAGGATCCTCGTGCCAGCGCGGCAATCGTCGCCCAAGATCGACG 908
182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPhe 201
909 ATTTCGAGCGCCAGCTCATCCAAACAACCTCGACCCAGGCACCTGCTGCTTCG 968
202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSe 221
969 GACAGCGAATGGCCCATACCGTCGAGCAAAATTCACGCCACGCTCGTCCCTCC 1028
222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValTh 241
1029 CGTCAAGCTCTGGAGAACGACCTGTCGGGTGTGACTCTCACAGACACAGAAGT 1088
242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLe 261
1089 CTCATGGACATGTGCTCTTCGACACCATCTCCACGACGCCCGTCCGACACAG 1148
262 ProPheCysAspLeuPheThrHisAspGluTyrIleAsnTyrAspTyrLeuGln 281
1149 CCCTTCTGTGACCTGTTCACCCATGACATGGATCACTACGACTACCTCCAGT 1208
282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValG 301
1209 AAAAAGTATTACGGCCATGGTGCAGGTAAACCGCTCGGCCGCCACCCAGGGCG 1268
302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSer 321
1269 GCTAACGAGCTCATCGCCCTCTGACCCACTCGCCCTCTCCAGATGACACAGT 1328
322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAla 341
1329 CACACTTTGGACTCGAGCCCGGTACCTTTCCGCTCAACTCTACTCTCTACGG 1388
342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGly 361
1389 TCGCATGACAAACGGCATCATCTCTCTTTGCTTTAGGTCTGTATCAACGGCAC 1448
362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSer 381
1449 CCGTATCTACCAACGCGGTGAGATATACCCAGACAGATGGATTTCTGCTGCTGG 1508
382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGlu 401
1509 ACGGTTCCGTTGCTTCGCGTTTGATCGTGAGATGATGAGTGTGAGCGGAGG 1568
402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysPro 421

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Db      1569  CCGCTGGTCCGCTGCTTGGTTAATGATCGCGTGTCCCGCTGCATGGGTGTCGGTGGAT 1628
QY      422  AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db      1629  GCTTTGGGAGATGTATACCGGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 1688
QY      442  GlyAspTrrAlaGluCysPheAla 449
Db      1689  GGTGATGGCGGAGTGTGTTGCT 1712

RESULT 4
US-10-662-914-21
; Sequence 21, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Millaney, Edward J
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLIUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 21
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-21

Alignment Scores:
Pred. No.: 1,036-271 Length: 2665
Score: 2350.00 Matches: 447
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.66% Indels: 0
DB: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-21 (1-2665)

QY      2  LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db      842  CTGGCAGTCCCGCTCGAAGATCAATCCAGTTGGATACGGTGCATCAGGGGTATCAA 901
QY      22  CysPheSerGluThrSerHisLeuTrrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db      902  TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGCACCGTTCTTCTCTGGGCAAC 961
QY      42  GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db      962  GAATCGGTCACTCCCTCGAGTGCCCGCGGATCGAGAGTCACATTCCTCTCGAGTCCCTC 1021
QY      62  SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
Db      1022  TCCCGTCAATGAGCGCGGTATCCGACCGACTCCAGGGGCAAGAAATCTCCGCTCTCAAT 1081
QY      82  GluGluIleGlnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db      1082  GAGGAGATCCAGCAGAACCGCACCTTTTGCGGAAATATGCTTCTCTGAAGACATAC 1141
QY      102  AsnTyrSerLeuGlyAlaAspSerLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db      1142  AACTACAGCTGGGTGCGATGACCTGACTCCCTTCGAGAACAGAGTAGTCAACTCC 1201
QY      122  GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db      1202  GGCATCAGTCTACACGGGTACGATCGATCGCTCACAGGAACATCGTTCCATTCATCGA 1261
QY      142  SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161

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Db      1262  TCCTCTGGCTCCAGCGCGTGCCTCCGCCAAGAAATTCATCGAGGGCTCCAGAGC 1321
QY      162  ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db      1322  ACCAAGCTGAAGAGATCCTCGTCCAGCCCGCCCAATCGTCCCAAGATCGACGTGGTC 1381
QY      182  IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db      1382  ATTTCCGAGGCCAGCTCATCCCAACACTCTCGACCCAGGCCACTGCTGCTCTCGAA 1441
QY      202  AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db      1442  GACAGCGAATTCGCCGATACCGTCCAAGCCAAATTCACCGCCACGTTGCTCCCTCCATT 1501
QY      222  ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGlnValThrTyr 241
Db      1502  CGTCAACGCTCTGGAGAACGACCTGTCGGGTGAGACTCTCACAGACACAGAAAGTACCTAC 1561
QY      242  LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db      1562  CTCATGGACATGTGCTCTCTCGACACCATCTCCACAGCACCGTGCACACCAAGCTGTCC 1621
QY      262  PropheCysAspLeuPheThrHisAspGluTrrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db      1622  CCCTTCTGTGACTGTTCAACCATGACGAATGATCAACTACGACTACCTCCAGTCTCTTG 1681
QY      282  LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db      1682  AAAAAAGTATTACGGCCATGGTGCAGGTAAACCGCTCGGCCCGGACCCAGGGCTCGGCTAC 1741
QY      302  AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db      1742  GCTACAGAGCTCATCGCCGCTCGACCATCTGCCCTGTCCAGATGACACAGTTCACAC 1801
QY      322  HisthrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db      1802  CACACTTTGGACTCGAGCCGGCTACCTTTTCGGCTCAACTCTACTCTCTACGCGGACTTT 1861
QY      342  SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db      1862  TCGCATGACAAAGCGCATCATCTCCATTCTCTTTGCTTTAGGTCTGTACAACGGCACTAAG 1921
QY      362  ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db      1922  CCGCTATCTACACGACCGTGGAGAAATATCACCCAGACAGATGGAATCTCTGCTCTCTGG 1981
QY      382  ThrValPropheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db      1982  ACGGTTCCGTTTGTCTTCGGTTTGTACGTCGAGATGATGAGTGTTCAGGCGGAGCAGAG 2041
QY      402  ProLeuValArgValLeuValAlaAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db      2042  CCGCTGGTCCCGTGTCTTGGTTAATGATCGCGTGTTCGCGCTGCATGGGTGTCGCGTTCAT 2101
QY      422  AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db      2102  GCTTTGGGAGATGTATCCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 2161
QY      442  GlyAspTrrAlaGluCysPheAla 449
Db      2162  GGTGATGGCGGAGTGTGTTGCT 2185

RESULT 5
US-10-662-914-27
; Sequence 27, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Millaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLIUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914

```



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; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-27

Alignment Scores:
Pred. No.: 1,03e-271 Length: 2665
Score: 2350.00 Matches: 447
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.66% Indels: 0
DB: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-27 (1-2665)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db 842 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAAGGGGTATCAA 901
QY 22 CysPheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db 902 TGCTTCTCCGAGACTTCGCAATCTTTGGGGTCAATACGACCGTCTCTCTCTGGCAAC 961
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 962 GAATCGGTATCTCCCTGAGGTGCGCGCGATGACAGAGTCACTTTCCGTCAGGTCCTC 1021
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
Db 1022 TCCCGTATGAGCGCGGTATCCGACCGACTCCAAAGGGCAAGAAATATCCGCTCTCAT 1081
QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 1082 GAGGAGATCCAGCAAGACGACACCTTTGACGGAAATATGCTTCTCTGAACATAC 1141
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGlnGlnLeuValAsnSer 121
Db 1142 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGAGAACAGGAGCTAGTCAACTCC 1201
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 1202 GGCAATCAAGTTCTACCAAGCGGTACGAATCGCTCAAGGAACATCGTTCCATTTCGGA 1261
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db 1262 TCCTCTGGCTCCAGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGTTCCAGAGC 1321
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 1322 ACCAAGCTGAAGGATCCTCGTCCGAGCGCGCAATCGTCCGCAAGATCGAGTGTGTC 1381
QY 182 IleSerGluAlaSerSerSerAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db 1382 ATTTCCGAGGCGACGCTCATCCAAACACACTCTCCAGCCAGGACCTGCGACTGTCTTCGAA 1441
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db 1442 GACAGCAATTTGGCGGATACCGTCCAGACCAATTTCCCGCACCTTGTCTCCCTCCATT 1501
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db 1502 CGTCAACGTCCTGGAGAACGACTGTCTCCGGTGTGACTCTCACAGACACAGAAAGTGACCTAC 1561
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrThrValAspThrLysLeuSer 261
Db 1562 CTCATGGACATGTGCTCTTGCACCACTATCCACCAACCGTCCAGACCAAGCTGTCC 1621

; Sequence 7, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-7

Alignment Scores:
Pred. No.: 1.35e-271 Length: 2665
Score: 2349.00 Matches: 447
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.62% Indels: 0
DB: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-7 (1-2665)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
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Db 842 CTGGAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGGTGATCAA 901
 QY 22 CysPheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaasn 41
 Db 902 TGCCTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCCGTTCTTCTCTGGCAAC 961
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 962 GAATCGGTCACTCCGCTGAGGTGCCCGCGATGCAGAGTCACATTCGCTCAGTCTCTC 1021
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysIleSerAlaLeu 81
 Db 1022 TCCCGTCATGAGCGCGGTATCCGACCGACTCAAGGGCAAGAAATCTCCGCTCTCAT 1081
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 1082 GAGGAGATCCAGACACGACACCTTTGACGGAATAATATGCTTCTTGAAGACATAC 1141
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluValAsnSer 121
 Db 1142 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGACAGGAGTAGTCACTCC 1201
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 1202 GGCAATCAAGTTCTACACGCGGTACGAATCGCTTCAAGGAAACATCGTTCCATTCGGA 1261
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 1262 TCCTCTGCTCCAGCGCGGTATCCCTCCGCGAAGAAATCATCGAGGCTTCCAGAGC 1321
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 1322 ACCAAGCTGAAGATCTCTGTCGCCAGCCCGCCAAATCGTCGCCCAAGATCGAGTGTG 1381
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrIleAspProGlyThrCysThrValPheGlu 201
 Db 1382 ATTTCCGAGGCGAGCTCATCCAAACAACTCTCGACCCAGGCACTGCTGACCTGTCTCGAA 1441
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 1442 GACAGCGAATTTGGCGATACCGTGAAGCCAAATTTACCGCCAGCTTCGTCCTCCCAT 1501
 QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 1502 CGTCAAAGTCTGGAGAACGACTGTCGGGTGACTCTCACAGACACAGAGTGCCTAC 1561
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 1562 CTCAATGACATGTGCTCTTCGACACCACTCTCCACGACCGCTCGACCAAGCTGTCC 1621
 QY 262 ProPheCysAspLeuPheThrHisAspGluThrIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 1622 CCTTCTGTGACCTGTCCACCATGACGAAATGGAATCAACTACGACTACTCCAGTCCCTG 1681
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 1682 GAAAGATATTACGGCATGTGTGAGTAACCCGCTCGGCCCGACCCAGGGGTGCGCTAC 1741
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 1742 GCTAACGAGCTCATCGCCCGCTGTACCCACATCTGCTCCAGATGACACCAAGTTCACAC 1801
 QY 322 HisThrLeuAspSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 1802 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTACCGCGGACTTT 1861
 QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1862 TCGCATGACACGGAATCATCTCCATCTCTTTGCTTAGTCTGTATCAACGGGCACTAAG 1921
 QY 362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381

Db 1922 CGCTATCTTACCACGCGTGGAGAAATATCACCCAGACAGATGGATTTCTGCTGCTGG 1981
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnIleGlnGlu 401
 Db 1982 ACGGTTCGCTTTCGCTTCGCTTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT 2041
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 2042 CGCTGGTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCG 2101
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 2102 GCTTTGGGAGATGTACCCGGGATAGCTTTGTAGGGGCTTGAGCTTTGCTAGATCTGG 2161
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 2162 GGTGATGGCGGAGTGTTCCT 2185
 RESULT 7
 US-10-662-914-17
 ; Sequence 17, Application US/10662914
 ; Publication No. US20040126844A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lei, Xingen
 ; APPLICANT: Mullaney, Edward J
 ; APPLICANT: Ullah, Abul H.J.
 ; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
 ; FILE REFERENCE: 19603/4261
 ; CURRENT APPLICATION NUMBER: US/10/662,914
 ; CURRENT FILING DATE: 2003-09-15
 ; PRIOR APPLICATION NUMBER: 60/410,736
 ; PRIOR FILING DATE: 2002-09-13
 ; NUMBER OF SEQ ID NOS: 69
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 17
 ; LENGTH: 2665
 ; TYPE: DNA
 ; ORGANISM: Aspergillus niger
 US-10-662-914-17
 Alignment Scores:
 Pred. No.: 1,35e-271 Length: 2665
 Score: 2349.00 Matches: 447
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.78% Mismatches: 0
 Query Match: 99.62% Indels: 0
 DB: 17 Gaps: 0
 US-10-089-364-4 (1-449) x US-10-662-914-17 (1-2665)
 QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 Db 842 CTGGAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGGTGATCAA 901
 QY 22 CysPheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaasn 41
 Db 902 TGCCTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGTTCTTCTCTGGCAAC 961
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 962 GAATCGGTCACTCCGCTGAGGTGCCCGCGATGCAGAGTCACATTCGCTCAGTCTCTC 1021
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysIleSerAlaLeu 81
 Db 1022 TCCCGTCATGAGCGCGGTATCCGACCGACTCCGAGGCAAGAAATCTCCGCTCTCAT 1081
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 1082 GAGGAGATCCAGACACGACACCTTTGACGGAATAATATGCTTCTTGAAGACATAC 1141
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluValAsnSer 121
 Db 1142 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGACAGGAGTAGTCACTCC 1201

122 GlyIleLysPheTyrlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
1202 GGCATCAAGTTCTACAGCGGTACGAATCGCTACAGGAACATCGTTCCATTCATCCGA 1261
142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161
1262 TCCTCTGGCTCCAGCGCGGTGATCGCTCGGCAAGAAATTCATCGAGGCTCCAGAGC 1321
162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
1322 ACCAAGCTGAAGATCCTCGTCCAGCGGCAATCGTCCGCCAAGATCGACGTGTC 1381
182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
1382 ATTTCCGAGGCGAGCTCATCCAAACACTCTCGACCCAGGACCTGCACTGTCTCGAA 1441
202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
1442 GACAGCGAATGGCCGATACCGTCCGAAGCCAAATTTCAACGCCACGTTGTCCTCCATT 1501
222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrIleuThrAspThrGluValThrTyr 241
1502 CECTCAACGCTCGAGAACACCTGTCGGGTGACTCTCACACACACAGAAAGTGCCTAC 1561
242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
1562 CTCATGGACATGTCCTCTCCGACCATCTCCACGACGACCTGCACACCAAGCTGTCC 1621
262 ProPheCysAspLeuPheThrHisAspGluTrrIleAsnTyrAspTyrLeuGlnSerLeu 281
1622 CCCTTCTGTGACCTGTTCCCATGACGAATGATCAACTACGACTACCTCCAGTCTCTG 1681
282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
1682 AAAAAATATTACGGCATGTGTCAGGTAAACCGCTCGGCCCGACCCAGGCGGTGCTAC 1741
302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
1742 GCTAACAGGCTCATPCGCCGCTGTGACCCACTCGCCTGTGCACGATGACACAGTCCAAC 1801
322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
1802 CACACTTTGGACTCGAGCCCGGTACTCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1861
342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
1862 TCGCATGACAAACGGCATCATCTCCATTTCTCTTTAGGTCTGTACAAACGGCACCTAAG 1921
362 ProLeuSerThrThrThrValGluAlaAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
1922 CGCTATCTACACAGCCGTTGGAGATATATCCACGACAGATGATGATTTCTCTGTCTGG 1981
382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
1982 ACGETTCGGTTTCTTCGCGTTTGTAGTCTGAGATGATGATGCTCAGGCGGAGCAGAG 2041
402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
2042 CCCTGTGTCTGCTCTCTGTTTAAATGATCGCGCTTTGTCCCGTGCATGGGTGTGCGGTGAT 2101
422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
2102 GCCTTGGGGAGATGATCCCGGATAGCTTTGTGAGGGGGTTGAGCTTTGTAGATCTGGG 2161
442 GlyAspTrpAlaGluCysPheAla 449
2162 GGTGATTGGCGGAGTGTGTTTGTCT 2185

RESULT 8

US-10-662-914-19

; Sequence 19, Application US/10662914

; Publication No. US2004012684A1

GENERAL INFORMATION:

; APPLICANT: Lei, Xinggen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.

; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES

; FILE REFERENCE: 19603/4261

; CURRENT APPLICATION NUMBER: US/10/662,914

; CURRENT FILING DATE: 2003-09-15

; PRIOR APPLICATION NUMBER: 60/410,736

; PRIOR FILING DATE: 2002-09-13

; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 2665

; TYPE: DNA

; ORGANISM: Aspergillus niger

US-10-662-914-19

Alignment Scores: 1.35e-271 Length: 2665

Pred. No.: 2349.00 Matches: 447

Score: 2349.00 Conservative: 1

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 99.78% Indels: 0

Query Match: 99.62% Gaps: 0

DB: 17

US-10-089-364-4 (1-449) x US-10-662-914-19 (1-2665)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
DB 842 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTGGATACGGTGCATCAGGGGTATCAA 901
QY 22 CysPheSerGluThrSerHisLeuTrrPlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
DB 902 TGTCTTCGAGACTTCGATCTTTGGGTCAATACGCACCGTCTCTCTCTGGCAAC 961
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
DB 962 GAATCGGTTCATCTCCCTGAGGTGCGCGGATGCAGAGTCACTTTCGTACAGTCTC 1021
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
DB 1022 TCCCGTCATGAGCGGGTATCCGACCGACTCCAGGGCAAGAAATACTCCGTCTCAT 1081
QY 82 GluGluIleGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
DB 1082 GAGGATCCAGCAGAACCGGACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 1141
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
DB 1142 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGGAGCTAGTCACTCC 1201
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
DB 1202 GGATCAAGTTCATCAGCGGTACGAATCGCTCAGGCAAGAAATTCATCGAGGCTCCAGAGC 1261
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161
DB 1262 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGCTCCAGAGC 1321
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
DB 1322 ACCAAGCTGAAGATCCTCGTCCCGACCGCGCAATCGTCGCCCAAGATCGACGTGTC 1381
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
DB 1382 ATTTCCGAGGCGAGCTCATCCAAACACTCTCGACCCAGGACCTGCACTGTCTTCGAA 1441
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
DB 1442 GACAGCGAATGGCCGATACCGTCCGAAGCCAAATTTCAACGCCACGTTGTCCTCCATT 1501
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241

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Db      1502 CGTCAACGCTCGAGAACGACCTGTCGGGTGACTCTCACAGACACAGAAAGTGACCTAC 1561
QY      242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db      1562 CTCATGGACATGCTTCCTCGAACCATCTCCACAGACCCGTCGACACCAAGCTGTCC 1621
QY      262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db      1622 CCCTTCTGTGACCTGTTACCCATGACGAATGATCACTACGACTCTCCAGTCTCTTG 1681
QY      282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db      1682 AAAAAGATTATACGGCCATGCTGAGGTGAGGTAAACCCGCTCGGCCGACCCAGGGCGTGGCTAC 1741
QY      302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db      1742 GCTACAGAGCTCATCGCCGCTGACCCACTCGCCCTGTCACGATGACACCGAGTCCAAAC 1801
QY      322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db      1802 CACACTTTGGACTCGAGCCGCGGTACTCTTTCCGCTCAACTCTCTACGCGGACTTT 1861
QY      342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db      1862 TCGCATGACAAACGGCATCATCTCCATTCTCTTTAGTCTGTACCAACGGCACTAAG 1921
QY      362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db      1922 CGGCTACTACACGACCGGTGAGAAATATACCCAGACAGATGATTCGCTCTGCTGG 1981
QY      382 ThrValProPheAlaSerArgLeuTyrValGluMetGlnCysGlnAlaGluGlnGlu 401
Db      1982 ACGGTTCCGTTTGCTCGCGTTGTACGTCGAGATGATGATGATGATGATGATGATGAT 2041
QY      402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db      2042 CCGCTGGTCCGCTGCTGCTGTTATGATCGCGTGTCCGCTGATCGGCTGCTGAT 2101
QY      422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db      2102 GCTTTGGGAGATGATACCCGGATGATGATGATGATGATGATGATGATGATGATGAT 2161
QY      442 GlyAspTrpAlaGluCysPheAla 449
Db      2162 GGTGATTGGCGAGTGTGCT 2185

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RESULT 9

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US-10-662-914-23
; Sequence 23, Application US/10662914
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLIUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 23
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-23

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Alignment Scores:

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Pred. No.: 1,35e-271 Length: 2665
Score: 2349.00 Matches: 447
Percent Similarity: 100.00% Conservative: 1

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Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.62% Indels: 0
DB: 17 Gaps: 0

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US-10-089-364-4 (1-449) x US-10-662-914-23 (1-2665)

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QY      2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db      842 CTGGCAGTCCGCCCTCGAGAAATCAATCCAGTTGCGATACGGTCCGATCAGGGGTATCAA 901
QY      22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db      902 TGTCTTCCGAGACTTCGCATCTTTGGGTCATATACGACCGCTTCTTCTCTCTGGGCAAC 961
QY      42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db      962 GAATCGGTCTATCTCCCTGAGGTGCCCGCGGATGCGAGTCACTTTGCTCAGGTCCTC 1021
QY      62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
Db      1022 TCCGTCATGGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATACCTCCGCTCTCAT 1081
QY      82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db      1082 GAGGAGATCCAGCAGAACGCGACCACTTTGACGGAATATGCTTCTCTGAGACATAC 1141
QY      102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db      1142 AACTACAGCTTGGGTGCGAGATGACCTGCTCCGAGAAACAGAGCTAGTCAACTCC 1201
QY      122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db      1202 GGCATCAAGTTCTACAGCGGTACGAATCGCTCAACAGGAACATCGTTCCATTCATCCA 1261
QY      142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db      1262 TCCTCTGGCTCCAGCGCGGTGATCGCTCCCGCAAGAAATTCATCGAGGCTTCCAGAGC 1321
QY      162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db      1322 ACCAAGCTGAAGGATCCCTCGTCCCGCAGCCCGCAATCGTCCCAAGATCGACGTGTC 1381
QY      182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGln 201
Db      1382 ATTCGAGGCGAGCTCATCCAAACACTCTCGACCCAGGCACTCGTCCGCTGCTCTTCCA 1441
QY      202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db      1442 GACAGCGAATTTGGCGGATACCGTCAAAGCCCAATTTACCGCCACGTTCTGTCCTCCATT 1501
QY      222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db      1502 CGTCAACGCTCTGGAGAACGACCTGCTCCGGTGTGACTCTCAAGACACACAGAAAGTGAC 1561
QY      242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db      1562 CTATGACATGCTGCTCTTCGACCATCTCCACCGACCGCTCGACCAAGAGTGTGCC 1621
QY      262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db      1622 CCCCTTCTGTGACCTGTTCAACCATGACGAATGATCACTACGACTACCTCCAGTCTCTTG 1681
QY      282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db      1682 AAAAAGATTATACGGCCATGCTGAGGTGAGGTAAACCCGCTCGGCCGACCCAGGGCGTGGCTAC 1741
QY      302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db      1742 GCTAACGAGCTCATCGCCGCTGACCCACTCGCCCTGTCCACGATGACACAGTTCCAAC 1801
QY      322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db      1802 CACACTTTGGACTCGAGCCGCGGTACTCTTTCCGCTCAACTCTCTCTACGCGGACTTT 1861

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QY 342 SerHisAspAsnGlyTllelleSerlleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db 1862 TCGCATGACACGGCATCATCTCCATCTCTTTGCTTTTAGGCTGTGACACGGCATTAAG 1921
QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db 1922 CGCTATCTACACGACCGGTGGAGATATACCCACAGACAGATGATTCCTGCTGCTGG 1981
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db 1982 ACGGTTCCGTTCTCTTGGGTTAAGATCGGCTGAGATGATGATGATGATGATGATGATG 2041
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db 2042 CCCTCGGTCGCTCTCTGTTGTTAAGATCGGCTGAGATGATGATGATGATGATGATG 2101
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db 2102 GCTTGGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161
QY 442 GlyAspTrpAlaGluCysPheAla 449
Db 2162 GGTGATTGGCGGAGTGTGTTGCT 2185

RESULT 10
US-10-662-914-33
; Sequence 33, Application US/10662914
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-33

Alignment Scores:
Pred. No.: 1,35e-271 Length: 2665
Score: 2349.00 Matches: 447
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.62% Indels: 0
DB: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-33 (1-2665)
QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db 842 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTGCATCAGGGGTATCAA 901
QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db 902 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACACCGCTTCTTCTCTGCGAAC 961
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 962 GAATCGGTCATCTCCCTGAGGTGCGCCGGATGACAGTCACTTTCGTCAGGTCCTC 1021
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
Db 1022 TCCCGTCATGGCGCGGTATCCGCCGATCTCAAGGCGCAAAATACTCTCCGCTCTCAT 1081
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QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 1082 GAGGAGATCCAGCAGAACCGGACCACTTTGACGGAAATATATGCTTCTCTGAGACATAC 1141
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db 1142 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGAGAGTAGTCACTCC 1201
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 1202 GGCATCAAGTTCTACACGCGGTACGAATCGCTCACAGGAACATCGTTCATTCATCCGA 1261
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161
Db 1262 TCCTCTGGCTCCAGCCGCGTATCGCTCCGGCAAGAAATTCATCAGGGCTTCCAGAGC 1321
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 1322 ACCAAGCTGAAGATCTCTGTCGCCAGCCGCGCAATCGTCGCCCAAGATCCGAGTGGTC 1381
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db 1382 ATTTCGAGGCCAGCTCATCCAAACACTCTCGACCCAGGCACCTGCACCTGCTTCGAA 1441
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db 1442 GACAGCGAATTGGCCGATACCGTCGAAGCCAAATTCACGCCACGTTTCGTCCTCCAT 1501
QY 222 ArgGlnArgLeuGlnAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db 1502 CGTCAACGCTCGAGAACGACCTGTCCGGTGTGACTCTCACACACACAGAGTGACCTAC 1561
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db 1562 CTATGACATGTGCTCTTCGACCACTCTCCACAGCACCGTCGACACCAAGCTGTCC 1621
QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db 1622 CCCTTCTGTGACCTGTTTCACTCCATGCAATGATCACTACGACTACCTCCAGCTCTTG 1681
QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db 1682 AAAGAGTATTACGGCCCATGTGAGGTAAACCGCTCGGCCGACCCAGGGGCTCGGCTAC 1741
QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db 1742 GCTAACGAGCTCATCGCCGCTCTGACCACTCTGCGCTCTCCACGATGACACCGATTCCA 1801
QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db 1802 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1861
QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db 1862 TCGCATGACAAACGGCATCACTCCATCTCTTTGCTTTAGTCTGTGTGTAACACGGCACTA 1921
QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db 1922 CCGCTATCTACACGACCGTGGAGATATACCCACAGACAGATGAGATTCTGCTGCTTGG 1981
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db 1982 ACGGTTCCGTTTGTCTGCGTTTGTACGTCCAGATGATGATGATGATGATGATGATG 2041
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db 2042 CCGCTGGTCCGTTGCTTGGTTAATGATCGGCTGTGTCGCCGCTGATGGGTGCTCGGTTG 2101
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db 2102 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161
QY 442 GlyAspTrpAlaGluCysPheAla 449
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Db      2162 GGTGATTGGCGGAGTGTCTTGGCT 2185
RESULT 11
US-10-662-914-5
; Sequence 5, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-5
Alignment Scores:
Pred. No.:      2,366-271      Length:      2665
Score:          2347.00      Matches:    447
Percent Similarity: 99.78%      Conservative: 0
Best Local Similarity: 99.78%      Mismatches: 1
Query Match:    99.53%      Indels:    0
Db:             17          Gaps:       0
US-10-089-364-4 (1-449) x US-10-662-914-5 (1-2665)
QY      2  LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db      842 CTGGGAGTCCCGCGCTCGAGAATCAATCCAGTTGGATACGATCGAGGGTATCAA 901
QY      22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPheSerLeuAlaAsn 41
Db      902 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCCATACGACCGCTTCTCTCTCGCAAC 961
QY      42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db      962 GAATCGGTATCTCCCTGAGTGGCGCGCGATGACAGAGTCACTTCGCTCAGTCTCTC 1021
QY      62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
Db      1022 TCCCGTCAATGGAGCGCGGTATCCGACCGACTCCAAAGGGCAAGAAATACTCCGCTCTCATT 1081
QY      82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db      1082 GAGGAGATCCAGCAGAGACGCGACCACTTTGACGGAATAATATGCTTCTCGAAGACATAC 1141
QY      102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db      1142 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGAGCTAGTCACTCC 1201
QY      122 GlyIleLysPheTyrGluArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db      1202 GGCATCAAGTTCTACACGCGGTACGAATCGCTCAACAGGAACATCGTTCATTATCCGA 1261
QY      142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db      1262 TCCTCTGGCTCCAGCGGTGATCCCTCCCGCAAGAAATATCATCGAGGGCTTCAGAGC 1321
QY      162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db      1322 ACCAAGCTGAAGATCCTCGTCCCGAGCCCGGCAATCGTCCCAAGATGACGTGGTGC 1381
QY      182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201

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Db      1382 ATTTCCGAGCCAGCTCATCCAAACAACACTCTCGACCCAGGCACCTGCATGCTTTCGAA 1441
QY      202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db      1442 GACAGCGAATTGGCCGATACCGTTCGAAGCAATTTTCCCGCCACCGTTCGTCCCTCCATT 1501
QY      222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db      1502 CGTCAACGCTCGGAGAACACCTGTCGGTGTGACTCTCACAGACACAGAAGTGACCTAC 1561
QY      242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db      1562 CTATGAGCATGTGCTCTTCGACACCATCTCCACGACACCGTTCGACACCAAGCTGTCC 1621
QY      262 ProPheCysAspLeuPheThrHisaspGluTrpIleAsnTyrAspTyrIleGlnSerLeu 281
Db      1622 CCCTTCTGTGACTGTTCACCCATGACGAATGATCACTACACTACGACTACCTCCAGTCCCTTG 1681
QY      282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db      1682 AAAAGATTATAGGCATCGTGAGGTAAACCGCTCGGCCCGACCCAGGGCGGTGCGCTAC 1741
QY      302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db      1742 GCTAACGAGCTCATCGCCGTCTGACCCACTCGCTGTCCACGATGACACGAGTCCACAC 1801
QY      322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrIleuTyrAlaaspPhe 341
Db      1802 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1861
QY      342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db      1862 TGCATGACACAGCGCATATCTCCATTCTCTTTGCTTTAGTCTGTACACGGCACTAAG 1921
QY      362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db      1922 CGCTATCTACCCAGCACCGTGGAGAAATATCACCCAGACAGATGGATTTCTGCTCTCTGG 1981
QY      382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGlnGlu 401
Db      1982 ACGSTTCGGTTCGCTTCGCTTGTACGTCGAGATGATGATGATGATGATGATGATGATGAT 2041
QY      402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db      2042 CGCTGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2101
QY      422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db      2102 GCTTTGGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161
QY      442 GlyAspTrpAlaGluCysPheAla 449
Db      2162 GGTGATTGGCGGAGTGTCTTGGCT 2185
RESULT 12
US-10-662-914-15
; Sequence 15, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 2665
; TYPE: DNA

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ORGANISM: Aspergillus niger
US-10-662-914-15

Alignment Scores: 2.36e-271 Length: 2665
Pred. No.: 2347.00 Matches: 447
Score: 2347.00
Percent Similarity: 99.78% Conservatives: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.53% Indels: 0
DB: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-15 (1-2665)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
DB 842 CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 901

QY 22 CysPheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsn 41
DB 902 TGGTTCTCCGAGACTTCGCACTTTTGGGGTCAATAGCACCGTTCCTCTCTGGCAAC 961

QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
DB 962 GAATCGGTCTATCCCTCGAGTGGCGCGCGGATGCGAGACTCACTTCGCTCAGGTCCTC 1021

QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
DB 1022 TCCCGTCATGAGCGCGGTATCCGACGACTCCCGGGCAAGAAATACTCCGCTCTCAT 1081

QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
DB 1082 GAGGAGATCCAGCAGACGGACCACTTTTGAAGAAATATGCTTCTCTGAACATAC 1141

QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGlnGlnValLeuValAsnSer 121
DB 1142 AACTACAGCTGGGTGCGAGATGACTGACTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 1201

QY 122 GlyTyrLeysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
DB 1202 GGATCAAGTCTTACCAAGCGGTAGCAATCGCTCAACAGGAACATCGTTCATTCATCGA 1261

QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
DB 1262 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCAGAGC 1321

QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
DB 1322 ACCAAGCTGAAGGATCCTCGTGGCCAGCCCGGCCAATCGTCGCCCAAGATCGAGCTGTC 1381

QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
DB 1382 ATTTCCGAGGCGAGCTATCCCAACAACTCTGACCCAGGACCTGCACTGTCTTCGAA 1441

QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
DB 1442 GACAGCAATTTGGCGGATACCGTGAAGCAATTTCAACCGCACGTTTCGTCCTCCATT 1501

QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
DB 1502 CGTCAACGCTCGGAGAACGACCTGTCGGGTGTGACTCTCAACAGACACAGAAAGTGACCTAC 1561

QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
DB 1562 CTCATGGACATGTGCTCTTCGACACCACTCTCCACGACCGTCGACCAAGCTGTCC 1621

QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
DB 1622 CCCTTCTGTGACCTGTTCAACCATGACGAATGGATCAACTACGATACCTCCAGTCCCTG 1681

QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
DB 1682 AAAAAAGTATTACGGCATGGTGCAGGTAAACCGCTCGGCCGACCCAGGGCGTCCGCTAC 1741

QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
DB 1742 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCCTGTCCAGATACACCAAGTTCACAC 1801

QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
DB 1802 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCACTCTACTCTCTACCGGGACTTT 1861

QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
DB 1862 TCGCATGACACCGCATCACTCCATCTCTTTGCTTAGTCTGTACAAACGGCACTAAG 1921

QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
DB 1922 CCGCTATCTACACGACCGTGGAGAAATATCACCCAGACAGATGGATTCGCTCTGTGG 1981

QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
DB 1982 ACGGTTCCGGTTTCGCTTCGCGGTTTGTACGTCAGATGATGCAGTGTGAGGGGAGCAGGAG 2041

QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
DB 2042 CCCTGGTCCGCTCTCTGGTTATGATCGGTTTCGCGCTGCATGGGTGTCGGGTTGAT 2101

QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
DB 2102 GCTTTGGGAGATGTATCCCGGATAGCTTTGTGAGGGGTGAGCTTTGCTAGATCTGGG 2161

QY 442 GlyAspThrAlaGluCysPheAla 449
DB 2162 GGTGATTTGGCGGAGTGTTTTGCT 2185

RESULT 13
US-10-662-914-29
; Sequence 29, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xinggen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-29

Alignment Scores: Length: 2665
Pred. No.: 2347.00 Matches: 447
Score: 2347.00
Percent Similarity: 99.78% Conservatives: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.53% Indels: 0
DB: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-29 (1-2665)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
DB 842 CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 901

QY 22 CysPheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsn 41
DB 902 TGGTTCTCCGAGACTTCGCACTTTTGGGGTCAATAGCACCGTTCCTCTCTGGCAAC 961

QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61

Db 962 GAATCGGTATCTCCCTCGAGGTGCCCGCGGATGAGAGTCATCTTTCGGCTCAGGTCCCTC 1021
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuLeu 81
Db 1022 TCCCGTCATGAGCGCGGTATCCAGCGATCCCAAGGGCAAGAAATATCCGCTCTCAT 1081
QY 82 GluGluLeuGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 1082 GAGGAGATCCAGCAGAAACGACCATCTTTGACGGAAATATGCTTCTCTGAAGACATAC 1141
QY 102 AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db 1142 AACTACAGCTTGGGTGCAGATGACCTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 1201
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 1202 GGCATCAAGTTCTACAGGGTACGAAATCGCTCACAGGAACATCGTTCCATTTCATCCGA 1261
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161
Db 1262 TCCTCTGGCTCCAGCGCGGTATCGCTCCGGCAAGAAATTCATCGAGGCTTCCAGAGC 1321
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 1322 ACCAAGCTGAAGGATCCTCGTCCCAAGCGCGGCAATCGTCGCCAAGATCGACGTGGTC 1381
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db 1382 ATTTCCGAGCGCAGCTATCCCAACAACTCTCGACCCAGGACCTGCTGCTTCGAA 1441
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db 1442 GACAGCGAATTGGCGATACCGCTCGAAGCCAAATTCACCGCCAGCTTCTGCCCTCCAT 1501
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db 1502 CGTCAACGCTCGAGAACACGCTCGCGTGTGACTCTCACAGACACAGAAAGTGCCTAC 1561
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db 1562 CTCATGGACATGTGCTCTTCGACACCATCTCCACAGCACCGCTGACACCAAGCTGTCC 1621
QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db 1622 CCCTTCTGTGACCTGTTCACCATGACGAATGATCACTACGACTACTTCAGTCCCTTG 1681
QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db 1682 ACAAGTATTACGGGCATGGTGCAGGTAAACCGCTCGGCCCGACCGCGCTCGGTAC 1741
QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerAsn 321
Db 1742 GCTAACAGACTCATCGCGCTGACCCACTCGCTGTCCAGATGACACAGATGTCCAAAC 1801
QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db 1802 CACACTTTGGACTCGAGCGCGGTACCTTTCGGCTCACTCTACTCTCTACGCGGACTTT 1861
QY 342 SerHisAspAsnGlyIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db 1862 TCGCATCAAGCGCATCATCTCCATTTCTTTTGGTCTGTAGTCTGTACACGGCACTAAG 1921
QY 362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db 1922 CGGTATCTACACAGCGGTGAGAAATATCCACAGACAGATGGATTCCTGCTGCTTGG 1981
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db 1982 ACGGTTCCGTTTGTCTTCGGTTTGTACGTTCAGATGATGCAGTGTACGGCGGAGCAGGAG 2041
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421

Db 2042 CCCTCGGTCCGTCTCTGGTTATGATCGCGTGTGCCCGTGCATGGGTGTCGGTTGAT 2101
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db 2102 GCCTTCGGGAGATGTATACCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGG 2161
QY 442 GlyAspTrpAlaGluCysPheAla 449
Db 2162 GGTGATTGGCGGAGTGTGTTGCT 2185
RESULT 14
US-10-662-914-31
; Sequence 31, Application US/1066291.4
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-31
Alignment Scores:
Pred. No.: 2,366-271 Length: 2665
Score: 2347.00 Matches: 447
Percent Similarity: 99.76% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.53% Indels: 0
DB: 17 Gaps: 0
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QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db 842 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGTCGATCAGGGGTATCAA 901
QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db 902 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGCTTCTTCTCTGSCAAC 961
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 962 GAATCGGTCTATCCCTGAGGTGCGCGCGATGACAGTCACTTCGCTCAGGTCTCTC 1021
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuLeu 81
Db 1022 TCCCGTCATGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATATCCGCTCTCAT 1081
QY 82 GluGluLeuGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 1082 GAGGAGATCCAGCAGAACCGCACCATCTTTCGCGGAAATATGCTTCTCTGAAGACATAC 1141
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db 1142 AACTACAGCTTGGGTGCAGATGACCTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 1201
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 1202 GGCATCAAGTTCTACAGGGTACGAAATCGCTCACAGGAACATCGTTCCATTTCATCCGA 1261
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161
Db 1262 TCCTCTGGCTCCAGCGCGGTATCGCTCCGGCAAGAAATTCATCGAGGCTTCCAGAGC 1321

162 ThrLeuLeuysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
1322 ACCAAGCTGAAGGATCCTGTCGCCCGCGGCAATCGTCGCCCAAGATCGAGCGGTC 1381
182 IleSerGluAlaSerSerAsnThrLeuAspProGlyThrCysThrValPheGlu 201
1382 ATTTCGAGGCCAGCTCATCCACACACTCTCGACCCAGGACCTGCACCTGCTTCGAA 1441
202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
1442 GACAGCGAATTGGCCGATACCGTCGAAGCCAAATTCACGCCACGTTGTCGCCCTCCATT 1501
222 ArgGluArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
1502 CGTCAACGCTCGAGAACGACCTGTCGGGTGTGACTCTCACACACAGAAAGTGACCTAC 1561
242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
1562 CTCATGGACATGTGCTCTTCGACACCATCTCCACACGACCGTCGACACCAAGCTGTC 1621
262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
1622 CCCTTCTGTACCTGTTCAACCATGACGAATGGATCAACTACGACTACCTCCAGTCCCTG 1681
282 LysIleTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
1682 GATAAGTATTACGGCCATGTGTCAGGTAACCGCTCGGCCCGACCCAGGGCGTCGGTAC 1741
302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
1742 GCTAACGAGCTCATCGCCGCTCTGACCCACTCGCCTCTCCACGATGACACCAAGTCCAAC 1801
322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
1802 CACACTTGGACTCGACCGCGGTACCTTTCGGCTCAACTCTACTCTCTAGCGGACTTT 1861
342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
1862 TCGCATGACACAGGCACTCATCTCACTCTCTTTGCTTTAGGTCGTGACACGGGACTAAG 1921
362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
1922 CCGCTATCTACACGCGTGGAGAAATATCACCACAGACAGATGATCTCGTCTGCTGG 1981
382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
1982 ACGGTTCCGTTGCTTCGCGTTTGTAGCTCGAGATGATGACAGTGTGTCAGGCGGAGAG 2041
402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
2042 CCGCTGGTCCGCTGCTTGGTTAAATGATGCGCTTGTCCGCTGCAATGGGTGTCGGTTGAT 2101
422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
2102 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGTAGATCTGGG 2161
442 GlyAspTrpAlaGluCysPheAla 449
2162 GGTGATTGGCGGAGTGTGTTGCT 2185

RESULT 15
US-10-662-914-11
; Sequence 11, Application US/10662914
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xinggen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abdul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLIUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15

; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-11
Alignment Scores: Length: 2665
Pred. No.: 3,11e-271 Matches: 447
Score: 2346.00
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.49% Indels: 0
Dbs: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-11 (1-2665)
QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db 842 CTGCGAGTCCCGCTCGAAGATCAATCCAGTTGGATACGGTCGATCAGGGGTATCAA 901
QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db 902 TGCTTCTCCGAGACTTCGCACTTTGGGGTCTATACGACCGCTTCTCTCTGGCAAC 961
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 962 GAATCGGTCACTCTCCCTGAGGTGCGCGCGATGACAGATCACTTTCGCTCAGGTCTC 1021
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
Db 1022 TCCGTCATCGAGCGCGGTATCCGACGACTCCCAAGGGCAAGAAATACTCGCTCTCAT 1081
QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 1082 GAGGAGATCCAGAGAACGCGACACCTTTGACGGAATAATGCTTCTTGAAGACATAC 1141
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db 1142 AACTACAGCTTGGGTGAGATGACCTGCTCCGAGAACAGAGAGTAGTCACTCC 1201
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 1202 GGCATCAAGTTCTACAGCGGTACGAATCGCTCAAGGAACATCGTTCATTCGAT 1261
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db 1262 TCCCTCTGGCTCCAGCGGTGATCGCTCCGCGCAAGAAATTCATCGAGGGCTTCCAGAGC 1321
QY 162 ThrIleLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 1322 ACCAAGCTGAAGATCTCTGTCGCCCGCGGCAATCGTCCGCCAAGATCGACGTGGTC 1381
QY 182 IleSerGluAlaSerSerSerAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db 1382 ATTTCGAGGCCAGCTCATCCACACACTCTCCGCCAGGACCTGCTGCTCTTCGAA 1441
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db 1442 GACAGCAATTTGGCCGATACCGTCGAAGCCAAATTCACGCCACGTTGTCGCCCTCCATT 1501
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db 1502 CGTCAACGCTCGAGAACGACCTGTCGGGTGTGACTCTCACACACAGAAAGTGACCTAC 1561
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db 1562 CTCATGGACATGTGCTCTTCGACACCATCTCCACACGACCGTCGACACCAAGCTGTC 1621
QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281

Db 1622 CCGCTTCTGTGACCTGTTCACCATGACGAATGGATCACTACGACTACCTCCAGTCCCTTG 1681
QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db 1682 AAAAGTATTACGGCCATCGTGCAGGTAAACCGCTCGGCCCGACCCAGGGCGTCCGCTAC 1741
QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db 1742 GCTAACGAGCTCATGCCCGCTGTGACCCACTCGCCTGTCCAGATGACACCATTCCTCAAC 1801
QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db 1802 CACACTTTGAGTCGAGCGCGCTACTTTTCGCTCACTCTACTCTCTACGGGACTTT 1861
QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db 1862 TCGCATGACACGGCATCATCTCCATCTCTTTAGGCTGTACACGGCACATAAG 1921
QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db 1922 CGGCTATCTACACGACCGTGGAGATATCACCCAGACAGATGGATTCTCGTCTGCTTGG 1981
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGlnGlu 401
Db 1982 ACGGTTCGGTTTGTCTCGCGTTTGTACGTGAGATGATCGAGTGTACGGCGGAGCAGGAG 2041
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db 2042 CGCTGTGTCGGTGTCTTGGTTAATGATCGCGTGTCCCGCTGCATGGGTCCGGTTGAT 2101
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db 2102 GCTTTGGGGAGATGTACCGGGGATAGCTTTGTGAGGGGTTTGCAGCTTTGCTAGATCTGGG 2161
QY 442 GlyAspTrpAlaGluCysPheAla 449
Db 2162 GGTGATTGGCGGAGTGTGTTTGTCT 2185

Search completed: October 24, 2004, 19:28:59
Job time : 844 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 13:06:14 ; Search time 5508 Seconds
(without alignments)
2970.486 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MIAVAFNRQSCDVTVDQY.....SFVRGLSFARSGDWAECFA 449

Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO.spool.p/US10089364/runat.22102004.184728.16282/app.query.fasta.1.647
-DB=BST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.gdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10089364 @CGN 1.1.6425 @runat.22102004.184728.16282 -NCPU=6 -ICPU=3
-NO.MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsl1.*
9: gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
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2	774.5	32.8	810	7	C0011644
C 3	721.5	30.6	880	7	C0004996
C 4	689.5	29.2	868	6	CD459861
C 5	634.5	26.9	737	7	C0011643
C 6	606	25.7	700	7	CK569249
C 7	575	24.4	802	8	AQ324539
8	547	23.2	603	1	AU248054
9	510	21.6	620	6	CD031252

C	10	450.5	19.1	586	6	CD030240
C	11	440	18.7	650	5	BQ142672
C	12	414	17.6	544	7	CF862369
C	13	387	16.4	581	1	AJ274007
C	14	387	16.4	1059	7	CN808226
C	15	374.5	15.9	837	8	AQ255459
C	16	368	15.6	526	6	CD056577
C	17	358	15.2	395	7	CN250089
C	18	326	13.8	510	4	BM866254
C	19	323.5	13.7	753	8	AQ163004
C	20	308	13.1	520	6	CD646039
C	21	302.5	12.8	669	8	AQ361495
C	22	296	12.6	275	5	BQ491147
C	23	296	12.6	1019	9	CNS07021
C	24	290	12.3	405	7	CN249954
C	25	288	12.3	691	6	CA747583
C	26	279.5	11.9	769	8	AQ361474
C	27	277.5	11.8	724	7	CF390509
C	28	273.5	11.6	1019	9	CNS0638E
C	29	267.5	11.3	978	9	CNS06N99
C	30	265	11.2	524	7	CF645025
C	31	261	11.1	699	8	AQ162040
C	32	260	11.0	963	9	CNS073L9
C	33	254	10.8	918	7	CF820741
C	34	253	10.7	810	8	AQ161556
C	35	245	10.4	787	9	CNS072VN
C	36	245	10.4	1110	9	CNS06FC9
C	37	244	10.3	922	9	CNS075LP
C	38	241	10.2	914	9	CNS075JG
C	39	240	10.2	746	6	CD645596
C	40	239	10.1	630	1	AJ273121
C	41	230.5	9.8	776	9	CNS07248
C	42	229.5	9.7	657	1	AJ635632
C	43	212.5	9.0	882	6	CD457694
C	44	210.5	8.9	690	5	BU062119
C	45	206	8.7	820	9	CG811687

ALIGNMENTS

RESULT 1
C0004997
LOCUS EST094997 934 bp mRNA linear EST 09-JUN-2004
DEFINITION Coccidioides posadasii sphere cdna library, 0.4 to 2.3
kb Coccidioides posadasii cdna clone CIEAM59 5' end, mRNA sequence.
ACCESSION C0004997
VERSION C0004997.1 GI:48511886
KEYWORDS EST.
SOURCE Coccidioides posadasii
ORGANISM Coccidioides posadasii
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
AUTHORS Onygenales; mitosporic Onygenales; Coccidioides.
Gardner, M.J. and Cole, G.T.
TITLE Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST793331
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
1..934
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"
/clone="CIEAM59"
/dev_stage="spherules"

FEATURES source

```
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA library,
0.4 to 2.3 kb"
/note="Vector: pExpress 1; Site 1: Not 1; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"
```

ORIGIN

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Alignment Scores:
Pred. No.: 9,41e-84 Length: 934
Score: 811.00 Matches: 150
Percent Similarity: 66.02% Conservative: 54
Best Local Similarity: 48.54% Mismatches: 105
Query Match: 34.39% Indels: 0
DB: 7 Gaps: 0

US-10-089-364-4 (1-449) x C0004997 (1-934)
QY 8 ArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCysPheSerGluThrSer 27
DB 4 AGACGAGATTGCAATGCACTAGTGTCAAGCTCGATACAGTGCACACGCGGTTTGCT 63
QY 28 HisLeuTropGlyGlnTyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerPro 47
DB 64 CAGCTCTGGGGCCAAATATTCCCGCTATTCTCTGAAAGTCAAAAGTCTCCCATCTCTCCG 123
QY 48 GluValProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyAlaArg 67
DB 124 GATGATACCGTCTGGATGCATATTACTTTTGGCCAAAGTCTGTCGGCGCATGGAGCAAG 183
QY 68 TyrProThrAspSerLysGlyLysTyrSerAlaLeuIleGlnGlnAsn 87
DB 184 TATCCACGAGAAAGAAACCGAGCTCTAGCAAACTCTTGATCGATCAAGAAACC 243
QY 88 AlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsnTyrSerLeuGlyAla 107
DB 244 AGCAAGTCTTATGAGGACGACTTCAAGTCTCTGAAAACTTTGAGTATACGCTGAAGAGC 303
QY 108 AspAspLeuThrProPheGlyGluGlnGluValAsnSerGlyIleLysPheTyrGln 127
DB 304 GATGATATGACAGAAATTCGGGACACCACTTCAATCTTGGGGCAAAATTTCTACGAT 363
QY 128 ArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSerSerGlySerArg 147
DB 364 CGCTATAGGGTTTGGCGAAGGATACGACCGTTCGTTCGAGTCGCGGGTCTCCGAGG 423
QY 148 ValIleAlaSerGlyLysLysPheIleGluGlnSerThrLysLeuLysAspPro 167
DB 424 GTGATCAAGTCAGCAGAGAGATTTATTCAAGGATTCAGAGATCTTGGGCGCTTGATCCT 483
QY 168 ArgAlaGlnProGlyGlnSerSerProLysIleAspValValIleSerGluAlaSerSer 187
DB 484 GATGGTGTGCGAAGGATAGACCCCTATCCTACACTTGATTTCCCTGAAGGAGAGTCG 543
QY 188 SerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAspSerGluLeuAlaAsp 207
DB 544 AGTAAACATACACTTGACCATCTTATCGGAAACCTTCGACAGGATAATTCAGGAAA 603
QY 208 ThrValGluAlaAsnPheThrAlaThrPheValProSerIleArgGlnArgLeuGluAsn 227
DB 604 GAGAAAGCAGAAAAAATTCGTGACCTATTTCGCCCTCCAAATTTCTTGACCGTGTGAAAAC 663
QY 228 AspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSer 247
DB 664 CATCTCCCTGGCGCAATATTACGTCACAGATGATCTACCTCATCGATATGTGCTCC 723
QY 248 PheAspThrIleSerThrThrValAspThrLysLeuSerProPheCysAspLeuPhe 267
DB 724 TTCCACACCGTATGTTGAGCGCCCGACGAGCAAACTATCTCCATTTCTGCCAACTCTTC 783
QY 268 ThrHisAspGluTyrIleAsnTyrAspTyrLeuGlnSerLeuLysLysTyrTyrGlyHis 287
DB 784 ACCCCAGGCGAATGGGTTGACTATGACTACTACCACTCTCTTGGGAAATATTTACAGATAT 843
```

```
QY 288 GlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAlaAsnGluLeuIleAla 307
DB 844 GGGCCAGGAGCCCGCTCGTGTGAGCAAGCATGGATTCACCAACGAACTCATAGCC 903
QY 308 ArgLeuThrHisSerProValHisasp 316
DB 904 CGTCTCACAACACACCCCGCTCAATGAC 930
```

```
RESULT 2
C0011644 810 bp mRNA linear EST 09-JUN-2004
LOCUS EST799979 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
DEFINITION kb Coccidioides posadasii cDNA clone CIEB041 5' end, mRNA sequence.
ACCESSION C0011644
VERSION C0011644.1 GI:48518533
KEYWORDS EST
SOURCE Coccidioides posadasii
ORGANISM Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 810)
AUTHORS Gardner,M.J. and Cole,G.T.
TITLE Analysis of gene expression in Coccidioides posadasii mycelia and
JOURNAL spherules via expressed sequence tags
COMMENT Unpublished (2003)
Other ESTs: EST799978
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Seq primer: M13 Reverse.
```

FEATURES

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source
1..810
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"
/clone="CIEB041"
/dev_stage="spherules"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA library,
0.4 to 2.3 kb"
/note="Vector: pExpress 1; Site 1: Not 1; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"
```

ORIGIN

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Alignment Scores:
Pred. No.: 1.43e-79 Length: 810
Score: 774.50 Matches: 145
Percent Similarity: 69.52% Conservative: 42
Best Local Similarity: 53.90% Mismatches: 79
Query Match: 32.85% Indels: 3
DB: 7 Gaps: 1
```

US-10-089-364-4 (1-449) x C0011644 (1-810)

```
QY 176 ProLysIleAspValValIleSerGluAlaSerSerSerAsnAsnThrLeuAspProGly 195
DB 3 CCTATCGTCACTTGATTTATCCCTCAAGAGAGAGTCAATACATACACTTGACACTCT 62
QY 196 ThrCysThrValPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThra 215
DB 63 TTATCGGAAACTTCGACACAGATAATTCAGNAAAGAGAGCAAAAAATTCGTGGAC 122
QY 216 ThrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThr 235
DB 123 CTATTTGGCCCTCCAAATTTCTGAGCGTGTGAAACTCATCTCCCTGGCGCAATATTACG 182
QY 236 AspThrGluValThrTyrLeuMetAspMetCysSerPheAspThrIleSerThrSerThr 255
```

```

Db      183  GTCACAGATGTGATACCTCATGGATATGTGCTCTCCACACCGTGATGTTGACGCC 242
QY      256  ValAspThrLysLeuSerProPheCysAspLeuPheThrHisAspGluThrPheLeuHis 275
Db      243  GAGCGAGCAGAACTATCTCATCTTCGCCAACTCTTCACCCAGCGAGTGGGTGACTAT 302
QY      276  AspTyrLeuGlnSerLeuLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyPro 295
Db      303  GACTACTACAGTCTCTTGGGAATATTACAGATATGGCCAGGCCCGCTCGTGCT 362
QY      296  ThrGlnGlyValGlyTyrAlaAsnGluLeuLeuAlaArgLeuThrHisSerProValHis 315
Db      363  GAGCAAGGATGGATGATTCACCAACGAACTCATAGCCCGTCTCACAAACACCCCGTCAAT 422
QY      316  AspAspThrSerSerAsnHisThrLeuAspSerProAlaThrPheProLeuAsnSer 335
Db      423  GACTCGACTTCACCAACCGCACTCTTACCTCTCACCCGACACCTTCCCGCTAAACGCC 482
QY      336  ThrLeuTyrAlaAspPheSerHisAspAsnGlyIleSerIleLeuPheAlaLeuGly 355
Db      483  ACTCTCTACGACAGCTTCAGCCATGATAACACTATGATAACGATCTTCACGCGCTTGGG 542
QY      356  LeuTyrAsnGlyThrLysProLeuSerThrThrValGluAsnIleThrGlnThrAsp 375
Db      543  CTGTTCAATPAGCAGCGAACCACTCCCTCTGACCGCATCCGGACCCCGCTAGAGTCGGAC 602
QY      376  GlyPheSerSerAlaThrThrValProPheAlaSerArgLeuTyrValGluMetGln 395
Db      603  GGATTTCTGCTGCTGGACGCTCCGTTTGCGGTAGGCGCTTACGTTGAGAAGTGAAG 662
QY      396  CysGln-----AlaGluGlnProLeuValArgValLeuValAsnAspArgVal 412
Db      663  TGTGACTGTGTCGCCAAGGAAGATGACGAGTTGTGAGAACTTCTGCTAAATGATGTT 722
QY      413  ValProLeuHisGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 432
Db      723  TATCCGCTCCATGGGTGTAACTGAGCTCATTAGCCGCTGCGAGTTAAATGATTTGTT 782
QY      433  ArgGlyLeuSerPheAlaArgSerGly 441
Db      783  AAGGGGCTGAGCTATGACGCGAGCGGG 809

```

```

RESULT 3
CO004996/c
LOCUS
DEFINITION
  EST793331 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
  kb Coccidioides posadasii cDNA clone C1EAM59 3' end, mRNA sequence.
ACCESSION
  CO004996
VERSION
  EST.
SOURCE
  CO004996.1 GI:48511885
  Coccidioides posadasii
  Coccidioides posadasii
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
  Onygenales; Mitosporic Onygenales; Coccidioides.

```

```

REFERENCE
  1 (bases 1 to 880)
  Gardner,M.J. and Cole,G.T.
  Analysis of gene expression in Coccidioides posadasii mycelia and
  spherules via expressed sequence tags
  Unpublished (2003)
  Other ESTs: EST793332
  Contact: Gardner MJ
  The Institute for Genomic Research
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301 838 3519
  Fax: 301 838 0208
  Email: gardner@tigr.org.
  Location/Qualifiers
    1..880
    /organism="Coccidioides posadasii"
    /mol_type="mRNA"
    /strain="C735"
    /db_xref="taxon:199306"

```

```

FEATURES
  source

```

```

/clone="C1EAM59"
/dev_stage="spherules"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA library,
0.4 to 2.3 kb"
/note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"

```

ORIGIN

```

Alignment Scores:
Pred. No.:      2,67e-73      Length:      880
Score:          721.50      Matches:      132
Percent Similarity: 73.80%      Conservative: 37
Best Local Similarity: 57.64%      Mismatches: 57
Query Match:      30.60%      Indels:      3
DB:              7          Gaps:      1

US-10-089-364-4 (1-449) x CO004996 (1-880)

QY      223  GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 242
Db      880  GAGCGTGTGAAAACTCATCTCCCTGGCGCAATATTACGTCACAGATGTGATCTACCTC 821
QY      243  MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 262
Db      820  ATGGATATGTGCTCTTTCACACCGTGATGTGACGCCGCGAGCAAACTATCTCCA 761
QY      263  PheCysAspLeuPheThrHisAspGluThrIleAsnTyrAspTyrLeuGlnSerLeuLys 282
Db      760  TTCTCCCAACTCTTCAACCCGCGGAATGGGTGACTATGACTACTACCACTCTCTGGG 701
QY      283  LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 302
Db      700  AAATATTACATATGCGCGACGAGCCGCTCGGTGTGAGCAAGGATGGGATTCACC 641
QY      303  AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 322
Db      640  AAGGNACTCATAGCCCGTCTCAAAACACACCCCGTCAATGACTCGACTTCACCAACCGC 581
QY      323  ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 342
Db      580  ACTCTTACCTCTCACCCGACCACTTCCCGCTTAACGCCACTCTCTACGACACTTCAGC 521
QY      343  HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 362
Db      520  CATGATAACATATATAACGATCTTCACGCGCTTGGGCGTGTTCATATAGCACGGAACA 461
QY      363  LeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaThrThr 382
Db      460  CTCCCGCTTGACCGATCCGGACCCCGTAGAGTCGGACGAGATTCTCGCTCGTGGACG 401
QY      383  ValProPheAlaSerArgLeuTyrValGluMetGlnCysGln-----AlaGlu 399
Db      400  GTCCCGTTCGCGGTAGGGCTTACGTTGAGAAGATGAAGTGTGACTGTCGCCAAGGAAG 341
QY      400  GlnGluProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysPro 419
Db      340  GATGACGAGTTTGTGAGAAATCTTCGTAATGATCGTGTGTTATCCGCTCCATGGGTGAAC 281
QY      420  ValAspAlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArg 439
Db      280  GTGGACTCATTAGCCCGGTGCGAGTTAAATGATTTGTTAAGGGGCTGAGCTATGCAGCG 221
QY      440  SerGlyGlyAspTrpAlaGluCysPhe 448
Db      220  AGCGGGGGAATGTGGACAGATGCTTT 194

```

```

RESULT 4
CD459861/c
LOCUS
DEFINITION
  FG09_07a12_A FG09 AAFc ECORC Fusarium graminearum simple_substrate
  Gibberella zeae cDNA clone FG09_07a12, mRNA sequence.

```



```

ACCESSION      CD459861
VERSION        CD459861.2
KEYWORDS       GI:48689893
SOURCE        Gibberella zeae
ORGANISM       Gibberella zeae
REFERENCE      1 (bases 1 to 868)
AUTHORS        Watson,R.J., Heyes,R., Couroux,P., De Moors,A., Harris,L.J.,
                Hattori,J.J., Lacroix,C., Masotti,M., Ouellet,T., Robert,L.S.,
                Singh,J.A., Sprott,D. and Tinker,N.A.
TITLE          A cDNA library prepared from Fusarium graminearum grown on a simple
                substrate
JOURNAL        Unpublished (2003)
COMMENT        On Jun 3, 2003 this sequence version replaced gi:31374601.
                Contact: Watson, Robert.J.
                Eastern Cereal and Oilseed Research Centre
                Agriculture and Agri-food Canada
                Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
                CANADA
                Tel: (613) 759-1655
                Fax: (613) 759-1701
                Email: watsonrj@agr.gc.ca.
FEATURES       Location/Qualifiers
                1..868
                /organism="Gibberella zeae"
                /mol_type="mRNA"
                /strain="DAOM 180378"
                /db_xref="taxon:5518"
                /clone="Pg09_07a12"
                /tissue_type="Mycelium"
                /dev_stage="Asexual"
                /lab_host="E. coli DH10B"
                /clone_lib="Pg09_AAPC_ECORC_Fusarium_graminearum_simple_su
                bstrate"
                /note="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
                XhoI; Fusarium graminearum grown on a simple substrate--
                minimal media supplemented with amino acids."
ORIGIN
Alignment Scores:
Pred. No.:      1,48e-69      Length:      868
Score:          689,50      Matches:    141
Percent Similarity: 64.86%      Conservative: 38
Best Local Similarity: 51.09%      Mismatches: 86
Query Match:     29.24%      Indels:    11
DB:              6          Gaps:       6

US-10-089-364-4 (1-449) x CD459861 (1-868)

Qy 180 valvalleserGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVal 199
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
842 CTGGTGATTCGGAAGAGTCGGGATCAACAACACCATGTCGATGCGATGATGATGCG 783
Qy 200 PheGlu--AspSerGluLeuAlaAspThr---ValGluAlaAsnPheThrAlaThrPhe 217
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
782 TTGAGAGAGACGACGACCTTGGCGATAACCAACCAACCGCTTGGGGAATAAGTTT 723
Qy 218 ValProSerLeuArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThr 237
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
722 CTGCTCCCATTCGAGACAGACTCAACAGAGATTGAAAGAGCGCAAGTTGTCGCTGAAG 663
Qy 238 GluValThrThrLeuMetAspMetCysSerPheAspThrIleSerThr-----SerThr 255
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
662 GAAACTGCTATCTCATGAGTCTGCGCTTCAACACCGCTCAACACCGCAACCCCGATGGCGCA 603
Qy 256 ValAspThrLysLeuSerProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyr 275
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
602 GTGCAGTCCAG-----TTTGGACCTCTTTCTACAGAAGATTGCGGAAGCTAC 552
Qy 276 AspTyrLeuGlnSerLeuLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyPro 295
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
551 AACTACTGGCAGACTCTCAGCAAGTACTACAAGTACGCGCAACGGGTAATGACATGGGACCA 492

```

```

Qy 296 ThrGlnGlyValGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHis 315
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
491 ACACAGGGTGTCGGATATGTTAATGAATCATCTCCGGCTGACACGAAGCCGTCAG 432
Qy 316 AspAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPheProLeuAsnSer 335
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
431 GATGACAACTACCAACACGACATTGGATTCCACCCAGAGAGCTTCCCTCTCGACAG 372
Qy 336 ThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGly 355
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
371 GCTCTGTATGCTGATTTTATGACCAACAGCATGTTTCCATCTTTCCGCTATGGGC 312
Qy 356 LeuTyrAsnGlyThrLysProLeuSerThrThrThrValGluAsnIleThrGlnThrAsp 375
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
311 CTGTACAACTACACAGGCAAGTTGCGAAACACCACTGTGCCAGCCGTCGGGGCGCAC 252
Qy 376 GlyPheSerSerAlaThrThrValProPheAlaSerArgLeuTyrValGluMetMetGln 395
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
251 GGCTACTCATCTGCGTGGTGGTCCCTTTTGGGGCGCGCATGTACCTCGAAGATCGAG 192
Qy 396 CysGlnAla-----GluGln-----GluProLeuValArgValLeuValAsnAspArg 411
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
191 TCGCGCGCCACCAAGAACAGAGGCGGAGTATGTGGGGTGTGTGTCATGACCGCA 132
Qy 412 ValValProLeuHisGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPhe 431
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
131 GTGATGGAGCTTGATACCTGTGGAGGAGATGAGTATGNNMTTGCATCTCTGGAAGACTTT 72
Qy 432 ValArgGlyLeuSerPheAlaArgSerGlyGlyAspTyrAlaGluCys 447
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
71 GTAGAGAGCTTGTGCTTTGCTAGAGAGGAGGACACTGGGATCGATGC 24

```

```

RESULT 5
COO11643/c
LOCUS     EST799978 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
DEFINITION kb Coccidioides posadasii cDNA clone CIEB041 3' end, mRNA sequence.
ACCESSION COO11643
VERSION    COO11643.1
KEYWORDS   EST.
SOURCE     Coccidioides posadasii
ORGANISM   Coccidioides posadasii
REFERENCE   1 (bases 1 to 737)
AUTHORS     Gardner,M.J. and Cole,G.T.
TITLE       Analysis of gene expression in Coccidioides posadasii mycelia and
            spherules via expressed sequence tags
JOURNAL     Unpublished (2003)
COMMENT     Other ESTs: EST799979
            Contact: Gardner MJ
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.
FEATURES   Location/Qualifiers
            1..737
            /organism="Coccidioides posadasii"
            /mol_type="mRNA"
            /strain="C735"
            /db_xref="taxon:199306"
            /clone="CIEB041"
            /dev_stage="spherules"
            /lab_host="E. coli DH10B, T1 phage resistant"
            /clone_lib="Coccidioides posadasii spherule cDNA library,
            0.4 to 2.3 kb"
            /note="vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
            Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
            kb"
ORIGIN

```

Alignment Scores:

Pred. No.: 3,216-63 Length: 737
 Score: 634.50 Matches: 115
 Percent Similarity: 75.39% Conservatives: 29
 Best Local Similarity: 60.21% Mismatches: 44
 Query Match: 26.91% Indels: 3
 DB: 7 Gaps: 1

US-10-089-364-4 (1-449) x CO011643 (1-737)

QY 261 SerProPheCysAspLeuPheThrHisAspGluTriPleAsnTyrAspTyrLeuGlnSer 280
 Db 737 TCTCCATTGCGCAACTCTCACCCAGGGAATGGTTGACTATACACTACTACCACTCT 678
 QY 281 LeuLysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGly 300
 Db 677 CTTGGGAATATTACAGATATGGCCAGGAGCCCGCTGGTCTGAGCAAGCATGGGA 618
 QY 301 TyrAlaAsnGluLeuLeuAlaArgLeuThrHisSerProValHisAspAspThrSerSer 320
 Db 617 TTTCAACAAGCAATCATAGCCGCTCTCAAAACACCCCGTCAATGACTCGACTTCCACC 558
 QY 321 AsnHisThrLeuAspSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAsp 340
 Db 557 AACCACACTCTTACCTCTCACCCAGCACCTTCCCGCTAAACGCCACTCTCTACGCAGAC 498
 QY 341 PheSerHisAspAsnGlyLeuLeuSerileLeuPheAlaLeuGlyLeuTyrAsnGlyThr 360
 Db 497 TTCAGCCATGATAACACTATGATACGATCTTCACGGCCTTGGGCTGTCTCATAGCACG 438
 QY 361 LysProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAla 380
 Db 437 GAACCACTCCCGCTTACCGCATCCGAGCCCGCTAGAGTCGAGCGGATTTCTGGCTCG 378
 QY 381 TrpThrValProPheAlaSerArgLeuTyrValGluMetGlnCysGln----- 397
 Db 377 TGGACGTCCCGCTTGGCGTGGGCTTACGTGAGAGATGAAGTGTGACTGTGCGCA 318
 QY 398 AlaGluGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuHisGly 417
 Db 317 AGGAAGGATGACGAGCTTTGTGAGATCTTGCTAAATGATCGTGTATCCGCTCCATGGG 258
 QY 418 CysProValAspAlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPhe 437
 Db 257 TGTACGTGGACTCATATTAGCCGCTGCGAGGTAAATGATTTGTAAAGGGCTGAGCTAT 198
 QY 438 AlaArgSerGlyGlyAspTyrAlaGluCysPhe 448
 Db 197 GCAGGACGGGGGAATGTGGACAGATGCTTT 165

RESULT 6

CK569249/c

LOCUS

DEFINITION HO12K16w HO Hordeum vulgare cDNA clone HO12K16 3-PRIME, mRNA

CK569249

VERSION CK569249.1

KEYWORDS EST.

SOURCE Hordeum vulgare

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.

1 (bases 1 to 700)

Zierold, U. and Schweizer, P.

Barley ESTs from pathogen-attacked leaf epidermis

Unpublished (2003)

Contact: Patrick Schweizer

Transcriptome Analysis, Cytogenetics Department

Institute of Plant Genetics and Crop Plant Research (IPK)

Corrensstr. 3, D-06466 Gatersleben, Germany

Tel: 0049 (0)39482-5660

Fax: 0049 (0)39482-5595

Email: schweiz@ipk-gatersleben.de
 Insert Length: 700 Std Error: 0.00
 Plate: 12 row: K column: 16
 Seq primer: T7.

FEATURES

source

Location/Qualifiers
 1..700
 /organism="Hordeum vulgare"
 /mol_type="mRNA"
 /cultivar="Ingrid BC mlo-5"
 /db_xref="GABI:903186"
 /db_xref="taxon:4513"
 /clone="HO12K16"
 /tissue_type="leaf epidermis, 6 h and 24 h post
 inoculation with Blumeria graminis"
 /dev_stage="7 d after germination"
 /lab_host="XL10-Gold"
 /clone_lib="HO"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
 cDNA); Site 2: XhoI (3'-end of cDNA); Approximately 5 % of
 the clones correspond to cDNA from the fungi B. graminis
 hordei and tritici, respectively. Due to a cloning
 artefact caused by the kit, in most cases the EcoRI site
 is NOT present, as well as the EcoRI adapter used for
 cloning. To excise the insert, restriction sites upstream
 EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
 due to the cloning system used Blue/white selection for
 recombinants is not 100% reliable. Average insert size is
 1.2 kb"

ORIGIN

Alignment Scores:
 Pred. No.: 6,5e-60 Length: 700
 Score: 606.00 Matches: 117
 Percent Similarity: 70.67% Conservatives: 30
 Best Local Similarity: 56.25% Mismatches: 57
 Query Match: 25.70% Indels: 4
 DB: 7 Gaps: 2

US-10-089-364-4 (1-449) x CK569249 (1-700)

QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 681 CTCATGGACCTTTGTCCTTTTGATACATTCACCAAGAA-----CAAGGTGAAGTCTCT 628
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 627 CCATTTCTCCATTTATTTCACCTGCTTCTGATGGCAGCGCTACGACTATATGAAACCGTT 568
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 567 GGAAGTACTACGGCTATTCATGGGGTAATCCCTGGAGCCACTCAGGGCGTGGTCTT 508
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 507 ACTAATGAGCTGATTGACGAGCTCCTCGCTCTCTCTCATCGATCACACAGACCAAT 448
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsn-----SerThrLeuTyrAla 339
 Db 447 AACACACTGATCATGACCAAAAGACATTTCTCTCGATAATCAAACTACTCTCTATGCC 388
 QY 340 AspPheSerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGly 359
 Db 387 GATTTTACGACGACCAACGACCTCCTAGTATATATGGCTGTGTGTGTCTCTACAAAGAT 328
 QY 360 ThrLysProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSer 379
 Db 327 TCTCCGCCACTCTCAAGACGACGCGTCCATCTTCAACGGCTACGACTATTCACCT 268
 QY 380 AlaTrpThrValProPheAlaSerArgLeuTyrValGluMetGlnCysGlnAlaGlu 399
 Db 267 AGCGGTACTGTACGTTTGGTGGCGGTATCTATTTCGAAAGTTGAAATGCCAAGATATA 208
 QY 400 GlnGluProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysPro 419

Db	207	GGGGAAGATTATCAGGAATATTGATGATCGGTTCTTCGCTCGAATCTTCGGGC	148
Qy	420	ValAspAlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArg	439
Db	147	GGAGATGAACCTGGGTAGGTACGCTAGATAAATTTGTGATAGCCTGAAATTTGGCGCA	88
Qy	440	SerGlyGlyAspTrpAlaGluCys	447
Db	87	CACGATGGAAGATGGTCTGAGTGT	64
RESULT 7			
AQ324539/c			
LOCUS		802 bp	DNA linear
DEFINITION		mgx0019C01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgx0019C01r, genomic survey sequence.	GSS 08-JAN-1999
ACCESSION		AQ324539	
VERSION		AQ324539.1	GI:4116391
KEYWORDS		GSS.	
SOURCE		Magnaporthe grisea (anamorph: Pyricularia grisea)	
ORGANISM		Magnaporthe grisea	
REFERENCE		1. (bases 1 to 802)	
AUTHORS		Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.	
TITLE		A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome	
JOURNAL		Unpublished (1998)	
COMMENT		Contact: Dean RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson University, Clemson, SC 29634 Tel: 864 656 5737 Fax: 864 656 4293 Email: rdean@clemson.edu Seq primer: GGAAACAGCTATGACCATG Class: BAC ends High quality sequence stop: 408. Location/Qualifiers 1. 802 /organism="Magnaporthe grisea" /mol_type="genomic DNA" /strain="70-15" /db_xref="taxon:148305" /clone="mgx0019C01r" /tissue_type="Protoplasts" /lab_host="E. coli DH10B" /clone_lib="CUGI Rice Blast BAC Library" /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII; Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."	
FEATURES		source	
ORIGIN			
Alignment Scores:			
Pred. No.:	3.47e-56	Length:	802
Score:	575.00	Matches:	110
Percent Similarity:	66.50%	Conservative:	27
Best Local Similarity:	53.40%	Mismatches:	65
Query Match:	24.3%	Indels:	4
Db:	8	Gaps:	2
US-10-089-364-4 (1-449) x AQ324539 (1-802)			
Qy	229	LeuSerGlyValThrLeuThrAspThrGluValThrTyLeuMetAspMetCysSerPhe	248

619 CTTAGAGGGTGAACCTCAGGCCAAGCGGTGCGATCATGAGCTTCGCCGCTT 560
249 AspThrIleSerThrThrValAspThrLysLeuSerProPheCysAspLeuPheThr 268
559 GAGACCGTGGCAGATCCN-----CAAGCCACCTGTCTGCAGTCTTCGACGCTGTTTACG 506
269 HisAspGluTrpIleAsnTyrAspTyrLeuInSerLeuLysLysTyrTyrGlyHisGly 288
505 CAACGAGACTGGGAGGCATATGATATCTCCAGACATCGGGAGTGGTATGGTTACGGC 446
289 AlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAlaAsnGluLeuAlaArg 308
445 AATGGCAACCCCTGGGCTCCACGCAAGGGTGGGCTTCGTCAACGAGCTCATCGGAGG 386
309 LeuThrHisSerProValHisAspThrSerSerAsnHisThrLeuAspSerSerPro 328
385 CTGCTCCAAAGCCCGTTGAAGACACACAAATACCACTCGAGCTCGACGAGGCCCA 326
329 AlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIlelle 348
325 TCGACGTTCCACTAGACAAAAAGCTGTACGCCGACTTTAGCCATGATACGATATGCTG 266
349 SerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrThrVal 368
265 GGCATCTACGCCCGCTGGGATTTACAGCCACGCGCCCGCCGATTCGGTCCCCAAAAG 206
369 Glu-----AsnIleThrGlnThrAspGlyPheSerAlaTrpThrValProPheAla 386
205 GAGAGAGGAGCGCGCAGGAGCTCAGCGGGTTCGTCCAGCTGGGGGTACCGTTCCGCA 146
387 SerArgLeuTyrValGluMetGlnCysGlnAlaGluGlnGluProLeuValArgVal 406
145 GCGAGGATGTTTGTGTAATAATGACTTGGCGAGGGCAGCAACGAGGAGCTTTGAGAAATC 86
407 LeuValAsnAspArgValValProLeuHisGlyCysProValAlaLeuGlyArgCys 426
85 CTGCTCAACGACAGGGTGCAGCGCTGCAGACTGCGATGCCGACATGGTGGTGGTGGTGC 26
427 ThrArgAspSerPheVal 432
25 ACGCTGAGCAAGTTCGTT 8
RESULT 8
AU248054
LOCUS AU248054 HL (Lolium multiflorum) Lolium multiflorum cDNA clone
DEFINITION AU248054 HL (Lolium multiflorum) Lolium multiflorum cDNA clone
ACCESSION AU248054.1 GI:46505323
VERSION AU248054.1
KEYWORDS EST.
SOURCE Lolium multiflorum (Italian ryegrass)
ORGANISM Lolium multiflorum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Poaceae; Lolium.
REFERENCE 1 (bases 1 to 603)
AUTHORS Ikeda, S.
TITLE Lolium multiflorum EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Seishi Ikeda
Japan Grassland Farming Forage Seed Association(JFSA)
Forage Crop Research Institute (FCRI)
Higashiakada 388-5, Nishinasuno, Tochigi 329-2742, Japan
Tel: 81-287-37-6755
Fax: 81-287-37-6757
Email: siked67@ffsaffr.or.jp
contact:Tadashi Takamizo (takamizo@affrc.go.jp)
National Institute of Livestock and Grassland Science, Nishinasuno
Resistance gene analog.
Location/Qualifiers
1. 603
/organism="Lolium multiflorum"

/mol_type="mRNA"
/db_xref="taxon:4521"
/clone="HL003E01-5"
/tissue_type="Heat shock leaf"
/clone_lib="HL (Lolium multiflorum)"

ORIGIN

Alignment Scores:

Pred. No.: 4.26e-53 Length: 603
Score: 547.00 Matches: 108
Percent Similarity: 69.31% Conservative: 32
Best Local Similarity: 53.47% Mismatches: 58
Query Match: 23.20% Indels: 4
DB: 1 Gaps: 2

US-10-089-364-4 (1-449) x AU248054 (1-603)

QY 224 ArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeuMet 243
Db 3 AGATTAGAGAAAACCTTGGCGGCACAGAATTTCCCGGAGCAGACAAATTCACATCATG 62
QY 244 AspMetCysSerPheAspThrIleSerThrValAspThrIleLeuSerProphe 263
Db 63 GACCTTGTCCGTTTGATACCATGTCTAATGAA-----CAAGGAGAGCTCTCCCATTT 116
QY 264 CysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 283
Db 117 TGCCACATATTCACTGCCCTCTGAATGGCGCGCTACGATTACTACCAACAGTTGGAAG 176
QY 284 TyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAlaAsn 303
Db 177 TACTACGGCTATTTCATGGGGTAATCCACTCGGACCCACTCAGGGGTCGGTTTACTAAT 236
QY 304 GluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHisThr 323
Db 237 GAGCTAATTGACGACTCACTCGCTCTCCCGTCATCGATCAGACGACCTAATACACA 296
QY 324 LeuAspSerSerProAlaThrPheProLeuAsnSer-----ThrLeuTyrAlaAspPhe 341
Db 297 CTCGACCAACAATCCCGAGGAGTTCTCTCGATAGCAAACTGCTTTACCGGACATT 356
QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db 357 AGCCACGACCAACGACCTCACTAGCATATTGGTGCAGTTGGTCTCTCAAAAATTTCTCG 416
QY 362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db 417 CCACCTCTCAAGACAGAGGTCCAATTTTAAAGCGAGTACGACTATTGCGACTAGCCGT 476
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db 477 ACTGTACCGTTCCGGTGGCGGTATCTATTTCGAAAATTGAAGTGCACAGATCTACGCA 536
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db 537 GATATGATACGGATATTGTGAATGATCGCGGTCTTCCACTTCAATCCTGTGGCGGAGAT 596
QY 422 AlaLeu 423
Db 597 GCATTG 602

RESULT 9
CD031252
LOCUS
DEFINITION
mgmt005xe03.f b Mated culture Magnaporthe grisea cDNA clone
VERSION
CD031252
KEYWORDS
EST.
SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 620)
Ebbole D.J., Yuan J., Thomas, T.L., Bobrowicz, P., Lu, G.,
Bhatnair, K. and Dean, R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe
grisea
Unpublished (2002)
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
personBest nr hit (April. 22, 2003) gb|AAB52508.1| phytase
[Thielavia heterothallica] 239 3e-62
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgmt005 row: E column: 03
Seq primer: T3
Location/Qualifiers
1..620
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="4091-5-8 X 4136-4-3"
/db_xref="taxon:148305"
/clone="mgmt005xe03"
/sex="Mat1-2 and Mat1-1 mixed culture"
/cell_type="mixed sexual development"
/dev_stages="asci, ascospores, perithecia, mycelium"
/clone_lib="Mated culture"
/note="Vector: pBluescriptSK; Site_1: EcoRI; Site_2: XhoI;
Two mating types were co-cultivated over a filter paper on
oatmeal agar medium. After three days at 25 C plates were
transferred to 21 C. Perithecia with asci and ascospores
formed at the beginning of the third week. Material was
collected by scraping tissue from the filter paper.
Sequences were processed by one of two methods. Where a
full-length alignment to the M. grisea genome sequence was
available, the EST sequence was trimmed according to the
alignment, otherwise sequence quality was assessed using
phredPhrap version 991019 and trimmed according to phd
files (0.05) and for vector seqs."

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 9.69e-49 Length: 620
Score: 510.00 Matches: 98
Percent Similarity: 64.39% Conservative: 34
Best Local Similarity: 47.80% Mismatches: 69
Query Match: 21.63% Indels: 4
DB: 6 Gaps: 2

US-10-089-364-4 (1-449) x CD031252 (1-620)

QY 190 AsnThrLeuAspProGlyThrCysThrValPheGluAspSerGluLeuAlaAspThrVal 209
Db 2 AACACGCTAAACCATACCTATGTACTCTTGAACACACAACTCGCAAGGAGCC 61
QY 210 GluAlaAsnPheThrAlaThrPheValProserIleArgGlnArgLeuGluAsnAspLeu 229
Db 62 CAAAAGAGTTATGGAGAGTGCCATGGCGGCATACAGAGCGCTTGAACACAGCGCTG 121
QY 230 SerGlyValThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAsp 249
Db 122 GAGGCTGCAACCTCCAGCACACGCGGTGAGATCATGGAGCTCTGCCCGTTGAG 181
QY 250 ThrIleSerThrSerThrValAspThrLysLeuSerPropheCysAspLeuPheThrHis 269
Db 182 ACCGTGGCAGATCCC-----CAAGCCACCTGTGCGAGTTCTGCACGCTGTTTACGCA 235
QY 270 AspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLysTyrTyrGlyHisGlyAla 289

oatmeal agar medium. After three days at 25 C plates were transferred to 21 C. Perithecia with asci and ascospores formed at the beginning of the third week. Material was collected by scraping tissue from the filter paper. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 91019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Alignment Scores: 8.4e-42 Length: 586
 Pred. No.: 450.50 Matches: 90
 Score: 450.50
 Percent Similarity: 68.55% Conservative: 19
 Best Local Similarity: 56.60% Mismatches: 48
 Query Match: 19.11% Indels: 3
 DB: 6 Gaps: 1

US-10-089-364-4 (1-449) x CD030240 (1-586)

Qy 292 ProLeuGlyProThrGlnGlyValGlyTyrAlaAsnGluLeuLeuAlaArgLeuThrHis 311
 Db 586 CCGCTGGGCTCCACGCAAGGGTGGGTTCGTCAACGAGCTCATCGAAGGTTC--TCA 529
 Qy 312 SerProValHisAspAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhe 331
 Db 528 AAGGCGTTGAGGCCACACAATACCACTCGACGCTCGACAGCAGCCATCGACGTTTC 469
 Qy 332 ProLeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyLleIleSerIleLeu 351
 Db 468 CCACTAGACAAAAAGCTGTACGCCGACTTTAGCCCATGATACCATATGCTGGGCACTAC 409
 Qy 352 PheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrThrThrValGlu---- 369
 Db 408 GCCGCGCTGGGGATTTACAACGCCGCCCGCCGATTCGGTCCCAAAAAGAAAGAGG 349
 Qy 370 AsnIleThrGlnThrAspGlyPheSerSerAlaTrpThrValProPheAlaSerArgLeu 389
 Db 348 AGCGCGCAGAAGCTACAGCGGGTTCCTCGTCAGCTGGCGGTACCGTTTCGACGAGGATG 289
 Qy 390 TyrValGluMetMetGlnCysGlnAlaGluGlnLupProLeuValArgValLeuValAsn 409
 Db 288 TTGTGTTCAAAAATGACTTCGCGAGGCGCAGAACGAGGAGCTTGTGAGAACTCTCGTCAAC 229
 Qy 410 AspArgValValProLeuHisGlyCysProValAspAlaLeuGlyArgCysThrArgAsp 429
 Db 228 GACAGGTGACGCCGCTGCAGAACTGCGATGCCACAGTAGTGGTCTGTTGCACGCTGAGC 169
 Qy 430 SerPheValArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPhe 448
 Db 168 AAGTTCGTTGAGAGCTTAAGCTTTGCGAGGAGTGGAGTTCGCTGGGATCAATGTTTT 112

RESULT 11

BQ142672

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

650 bp mRNA linear EST 24-APR-2002
 6 Metarhizium anisopliae sf. acridum ARSEF 324 Metarhizium
 anisopliae var. acridum cDNA, mRNA sequence.

BQ142672.1 GI:20279731

Metarhizium anisopliae var. acridum

Metarhizium anisopliae var. acridum

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Clavicipitaceae; mitosporic

Clavicipitaceae; Metarhizium.

1 (bases 1 to 650)

Freimoser, F.M., Screen, S., Baga, S., Hu, G. and St. Leger, R.J.

EST analysis of genes expressed by two different insect pathogenic

fungi during optimized secretion of proteins

Unpublished (2002)

Contact: Freimoser F. M.

Db 236 CGAGACTGGAGGCATATGACTATCTCCAGACACTGGGAGGTGATGTTACGGCAAT 295
 Qy 290 GlyAsnProLeuGlyProThrGlnGlyValGlyTyrAlaAsnGluLeuLeuAlaArgLeu 309
 Db 296 GGCACACCCCTGGGCTCCACGCAAGGGTGGGTTCGTCAACGAGCTCATCGGAGGCTG 355
 Qy 310 ThrHisSerProValHisAspAspThrSerSerAsnHisThrLeuAspSerSerProAla 329
 Db 356 CTCACAAAAGCCGTTGAGACCCACACAATACCACTCGACGCTCGACAGCAGCCATCG 415
 Qy 330 ThrPheProLeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyLleIleSer 349
 Db 416 ACCTTCCCATAGACAAAAAGCTAGCGCGACTTTCAGCATGATACGATATGCTGGGC 475
 Qy 350 IleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrThrThrValGlu 369
 Db 476 ATCTAGCGCGCTGGGGATTTACAGCCACGCGCCCGCATTCGGTCCCAAAAAGAG 535
 Qy 370 -----AsnIleThrGlnThrAspGlyPheSerSerAlaTrpThrValProPheAlaSer 387
 Db 536 AGAAGGAGCGGAGGAGCTCAGCGGGTTCGCGCAGCTGGGCGTACCGTTCGCGAGCG 595
 Qy 388 ArgLeuTyrValGlu 392
 Db 596 AGGATGTTGGTGAA 610

RESULT 10

CD030240/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD030240 586 bp mRNA linear EST 07-MAY-2003
 mgmt001x016f.b Mated culture Magnaporthe grisea cDNA clone
 mgmt001x016 5', mRNA sequence.

CD030240

CD030240.1 GI:30412076

EST.

Magnaporthe grisea (anamorph: Pyricularia grisea)

Magnaporthe grisea

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetes; incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 586)

Ebbels, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,

Bhatterai, K. and Dean, R.A.

Expressed sequence tags from the rice blast fungus, Magnaporthe

grisea

Unpublished (2002)

Contact: Ebbels DJ

Department of Plant Pathology & Microbiology

Texas A&M University

Peterson Bldg, MS2132, College Station, TX 77843-2132, USA

Tel: 979 845 4831

Fax: 979 845 6483

Email: d-ebbles@tamu.edu

Chromatogram file of this sequence is available, see contact

person; Best nr hit (April. 22, 2003) gb|AAB52508.1| phytase

[Thielavia heterothallica] 166 5e-44

PCR Primers

FORWARD: T3 primer

BACKWARD: T7 primer

Plate: mgmt001 row: 0 column: 16

Seq primer: T3.

Location/Qualifiers

1. 586

/organism="Magnaporthe grisea"

/mol_type="mRNA"

/strain="4091-5-8 X 4136-4-3"

/db_xref="taxon:148305"

/clone="mgmt001x016"

/sex="Mat1-2 and Mat1-1 mixed culture"

/cell_type="mixed sexual development"

/dev_stage="asci, ascospores, perithecia, mycelium"

/clone_lib="Mated culture"

/note="Vector: pBluescriptSK; Site_1: EcoRI; Site_2: XhoI;

Two mating types were co-cultivated over a filter paper on


```

QY 27 SerHisLeuTrpGlyGlnTyrAlaProPheSerLeuAlaAsnGluSerValIleSer 46
Db 432 CCACAGCACTGGGGCCAGTACTCGCGTACTTCTCA--GCACACAAGGATCTATTAG 488
QY 47 ProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyAla 66
Db 489 CCGTACATCCCGTCGGATGCGAGGTACCTTTGCTTCAATCTGCTCGACATGGTCC 548
QY 67 ArgTyrProThrAspSerIleGlyLysTyrSerAlaLeuIleGluLileGln 86
Db 549 CGCAACCGGACGGCGGCAAGTCCAAAGGCTTCAAGGACCTGTGAGCGGATCCAAAAA 608
QY 87 AsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsnTyrSerLeuGly 106
Db 609 GAGCTCAAGGACTATGGGAAGGGCTTCGAGTTTCTCAAGATTCAAGTACTTAGGT 668
QY 107 AlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGlyLysPheTyr 126
Db 669 TCTGACGACCTCACCCCTTGGGCGAGCAGGAATGGTCAAGTCTGGAAAAAAGTCTTC 728
QY 127 GlnArgTyrGluSerLeuThrArgAsnIleVal---ProPheIleArgSerSerGlySer 145
Db 729 AAGCCCTATCAAGAAGTATGCGGAGGATTCGACCCATCCCTTTGTTGAGCCCTCGGGCT 788
QY 146 SerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSerThrLysLeuLys 165
Db 789 GAAAGAGTGTGATCTACGCGCAAGATTTGTTCTATGGCTTCTCAAGGCCAAGGCGAAG 848
QY 166 Asp 166
Db 849 AAT 851

RESULT 15
AQ255459
LOCUS
DEFINITION
mgxb0014M15r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0014M15r, genomic survey sequence.
ACCESSION
AQ255459
VERSION
AQ255459.1 GI:3779774
KEYWORDS
GSS.
SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes; incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 837)
AUTHORS
Yu, Y.; Zhu, H.; Boyd, C.A.; Gaudette, B.; Gayle, A.; Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL
Unpublished (1998)
COMMENT
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel.: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 60
High quality sequence stop: 277.
FEATURES
Location/Qualifiers
1..837
/organism="Magnaporthe grisea"
/mol_type="genomic DNA"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0014M15r"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;"

```

Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

ORIGIN

```

Alignment Scores:
Pred. No.: 1,19e-32 Length: 837
Score: 374.50 Matches: 80
Percent Similarity: 55.67% Conservative: 28
Best local Similarity: 41.24% Mismatches: 69
Query Match: 15.88% Indels: 17
DB: 8 Gaps: 2

US-10-089-364-4 (1-449) x AQ255459 (1-837)
QY 223 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 242
Db 124 CAACGCATAGGCTGGGATTTTCAAGTGTCTGGGTTAACCGGTCAAGACGTTGTAATCTT 183
QY 243 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 262
Db 184 ATGGGACTGTGCACCATGGAAACAACGGCGAATCTTTGAAAAAATCTGGCCAACTTTCACCG 243
QY 263 PheCysAspLeuPheThrHisAspGluTyrIleAsnTyrAspTyrLeuGlnSerLeuLys 282
Db 244 CTTTGCAATCTGTTTACGGAACGAGATGGGTAATAATATGTTACTTGTCCACGCTGCAA 303
QY 283 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 302
Db 304 AAATGGTACAGATACGGAACGGTAATCTTTGGGCCCACTATGGCGCTGGGATGGGTA 363
QY 303 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 322
Db 364 AACGAACCTTATGTCACGATTAAACCGAAGCCGACGTCGAAGATCAACCATGTCCAAATACG 423
QY 323 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 342
Db 424 ACACCTTGACATGAACCCGGAACCTTACTCTACGAAGCAAAATTCATGCTGATTTATC 483
QY 343 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsn----- 358
Db 484 CATACGGACGATATATAGGGATTTACGCGCGGTTTGGGCTATTATTAACGCCCGCGCTTT 543
QY 359 GlyThrLysProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSer 378
Db 544 GGAAAAACAAAAATTTCCACCTATAAAATTCACCTCCATAGGACCTTGGTGGATTTTAT 603
QY 379 SerAlaTrpThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAla 398
Db 604 TCA-----ATATGAGATGCCATTG 624
QY 399 GluGlnGluProLeuValArgValLeuValAsnAspArgVal 412
Db 625 GGGCTAGAGATGTCGTTGAGAAAAATAATTTTCATCGGACATA 666

```

Search completed: October 24, 2004, 17:23:20
Job time : 5518 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 24, 2004, 11:03:13 ; Search time 115 Seconds
(without alignments)
1400.604 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MLAVPASRNQSCSDTVDQGY.....SFVRGLSFARSGDWAECEFA 449

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep 23Sep04: *
1: genesep1980s: *
2: genesep1990s: *
3: genesep2000s: *
4: genesep2001s: *
5: genesep2002s: *
6: genesep2003as: *
7: genesep2003bs: *
8: genesep2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	2358	100.0	449	4	AA72974	Aspergill
2	2358	100.0	482	4	AA72978	Aspergill
3	2353	99.8	448	5	ABB83811	Carrot ex
4	2353	99.8	467	2	AA111333	Aspergill
5	2353	99.8	467	2	AA111333	Recombina
6	2353	99.8	467	2	AA111333	Recombina
7	2353	99.8	467	2	AA111333	Recombina
8	2353	99.8	467	2	AA111333	Recombina
9	2350	99.7	467	8	ADL91242	Aspergill
10	2350	99.7	467	8	ADL91242	Aspergill
11	2349	99.6	467	8	ADL91262	Mutant ph
12	2349	99.6	467	8	ADL91260	Mutant ph
13	2349	99.6	467	8	ADL91264	Mutant ph
14	2349	99.6	467	8	ADL91274	Mutant ph
15	2349	99.6	467	8	ADL91248	Mutant ph
16	2347	99.5	467	8	ADL91258	Mutant ph
17	2347	99.5	467	8	ADL91272	Mutant ph
18	2347	99.5	467	8	ADL91270	Mutant ph
19	2347	99.5	467	8	ADL91256	Mutant ph
20	2346	99.5	467	8	ADL91245	Mutant ph
21	2346	99.5	467	8	ADL91266	Mutant ph
22	2346	99.5	467	8	ADL91266	Mutant ph
23	2345	99.4	467	8	ADL91280	Mutant ph
24	2345	99.4	467	8	ADL91276	Mutant ph
25	2343	99.4	467	8	ADL91309	Mutant ph

ALIGNMENTS

RESULT 1
AA72974
ID AA72974 standard; protein; 449 AA.
AC AA72974;
XX
XX
DT 13-JUN-2001 (first entry)
XX
DE Aspergillus niger phytase (Phy) A-1 protein.
XX
KW Phytase A; Phy; plant productivity; phosphorus utility;
KW biomass production; hypocotyl production; epicotyl production;
KW transgenic plant; phytate.
XX
OS Aspergillus niger.
XX
FN WO200122806-A1.
XX
PD 05-APR-2001.
XX
PE 22-SEP-2000; 2000WO-AU001183.
XX
PR 24-SEP-1999; 99AU-00003049.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (AUMO-) AUSTRALIAN WOOL RES & PROMOTION ORG.
XX
PI Richardson AE, Hayes JB, Simpson RJ;
XX WPI; 2001-244964/25.
DR N-PSDB; AAD03283.
XX
PT New isolated nucleic acid encoding a mature phytase polypeptide for
enhancing the phosphorus nutrition of a plant, the growth of a plant on a
phosphorus source and the phosphorus content of a plant.
XX
PS Claim 6; Page 124-126; 144pp; English.
XX
CC The invention relates to a method of modifying plant productivity which
involves expressing (Phy) A phytase gene from Aspergillus niger, in a
plant cell. Phytase gene is capable of facilitating plants ability to
utilize soil phosphorus. It is used to enhance the phosphorus nutrition
of a plant or the growth of a plant on a phosphorus source comprising
phytate and/or increase the phosphorus content of a plant. This gene is
used to enhance the biomass produced by a plant and also to enhance the
rate of hypocotyl production or the rate of epicotyl production.
CC Transgenic plant containing phytase gene has improved productivity than
its isogenic counterparts. The present sequence is Aspergillus niger Phy

1

AC ABB83811;
 XX 17-SEP-2002 (first entry)
 XX Aspergillus niger phyA related polypeptide 2.
 XX
 XX Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; enzyme.
 XX Aspergillus niger.
 OS
 XX
 PN CN1333363-A.
 XX
 PD 30-JAN-2002.
 XX
 PF 12-JUL-2000; 2000CN-00117245.
 XX
 PR 12-JUL-2000; 2000CN-00117245.
 XX
 PA (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.
 XX
 XX Chen Z, Yang L, Fang L;
 DR WPI; 2002-305615/35.
 DR N-PSDB; ABN85590.
 XX
 PT Phytase gene sequence and application in yeast thereof.
 XX
 PS Disclosure; Fig 4; 48pp; Chinese.
 XX
 CC The invention relates to a coded phytase gene sequence suitable for
 CC secretion and expression in yeast and its application. It is mainly
 CC characterised by removing nucleotide sequence of +45-+146 bit from phyA
 CC total length structure gene sequence, removing Aspergillus niger signal
 CC peptide coded sequence of +1-+44 and +147-+159, connecting a part of
 CC signal peptide code sequence suitable for secretion and expression at 5'
 CC end and connecting a restriction endonuclease site at 3' end. The
 CC different carriers can be connected into said gene sequence so as to form
 CC a recombinant plasmid with different functions and after the recombinant
 CC plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
 CC yeast, finally the invented Pasteur Pichia yeast engineering bacterium
 CC (CCTCC NO:M200005) can be obtained through the screening process. By
 CC using the invention the industrial process of phytase bio-expression can
 CC be successfully implemented. The present sequence is that of a
 CC polypeptide of the invention
 XX
 SQ Sequence 448 AA;

Query Match 99.8%; Score 2353; DB 5; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.7e-215;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPACGRVTFQVL 61
 DB 1 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPACGRVTFQVL 60
 QY 62 SRHGARYPTDSKGKYSALIEEIQONATTPDGKYAFLKTYNSLGADLTPFGQELVNS 121
 DB 61 SRHGARYPTDSKGKYSALIEEIQONATTPDGKYAFLKTYNSLGADLTPFGQELVNS 120
 QY 122 GIKFYQRYESTRNIVPFIRSSGSRVTSAGKKIEGFQSTKLDPRAQPGQSSPKIDVV 181
 DB 121 GIKFYQRYESTRNIVPFIRSSGSRVTSAGKKIEGFQSTKLDPRAQPGQSSPKIDVV 180
 QY 182 ISEASSNNITLDPCTCTVFEDESELADTVANFTATFVPSIRQLENDLSGVTLTDEVTY 241
 DB 181 ISEASSNNITLDPCTCTVFEDESELADTVANFTATFVPSIRQLENDLSGVTLTDEVTY 240
 QY 242 LMDMCSPTTISTSTVDTKLSPFCDLTFHDEWINYDYLQSLKYYGHGAGNPLGFTQGVY 301
 DB 241 LMDMCSPTTISTSTVDTKLSPFCDLTFHDEWINYDYLQSLKYYGHGAGNPLGFTQGVY 300
 QY 302 ANELIARLTHSPVHDDTSSNHTLSSPATPLNTLYADFSHNGIISILFALGLYNGTK 361

DB 301 ANELIARLTHSPVHDDTSSNHTLSSPATPLNTLYADFSHNGIISILFALGLYNGTK 360
 QY 362 PLSTTTVENITQDGFSSAWTVFFASRLYVEMMQCAEQEPLVRLVNDRVVPLHGCPVD 421
 DB 361 PLSTTTVENITQDGFSSAWTVFFASRLYVEMMQCAEQEPLVRLVNDRVVPLHGCPVD 420
 QY 422 ALGRCRTDSFVRGLSFARSGGDWAECEFA 449
 DB 421 ALGRCRTDSFVRGLSFARSGGDWAECEFA 448

RESULT 4
 AAR11333
 ID AAR11333 standard; protein; 467 AA.
 XX
 AC AAR11333;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-2000 (revised)
 DT 31-MAY-1991 (first entry)
 XX
 XX Recombinant chromosomal phytase.
 DE Microbial phytase; animal feeds; inositol; inorganic phosphates.
 KW
 XX Synthetic.
 OS
 XX EP420358-A.
 PN
 XX
 PD 03-APR-1991.
 XX
 PF 27-SEP-1990; 90EP-00202565.
 XX
 PR 27-SEP-1989; 89EP-00202436.
 PR 17-AUG-1990; 90EP-00202231.
 XX
 XX (KONN) GIST-BROCADES NV.
 PA (STAM) DSM NV.
 PA Van Gorcom RF, Van Hartingsveldt W, Vanparidon PA, Beenstra AE;
 PI Luiten RG, Seltten GCM;
 XX WPI; 1991-095799/14.
 DR N-PSDB; AAQ11175.
 XX
 PT DNA encoding phytase - used for recombinant expression for prodn. of
 PT phytase for conversion of phytate to inositol and inorganic phosphate
 PT esp. in animal feed.
 XX
 PS Disclosure; Fig 8; 61pp; English.
 XX
 CC This sequence is encoded by a DNA sequence deduced from comparisons of
 CC respective sequences of clones identified using oligonucleotide probes.
 CC The use of recombinant DNA methods for the the enzyme prodn. allows the
 CC large scale prodn. of proteins and peptides having phytase activity.
 CC These are used for the conversion of phytate to inositol and inorganic
 CC phosphate and can be used in industrial processes. The phosphate content
 CC of manure thus can be decreased. See also AAQ1157-74. (Revised record
 CC issued to correct errors present in the sequence portion of the original
 CC GENESQ entry.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 CC 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 467 AA;

Query Match 99.8%; Score 2353; DB 2; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.8e-215;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPACGRVTFQVL 61
 DB 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPACGRVTFQVL 79
 QY 62 SRHGARYPTDSKGKYSALIEEIQONATTPDGKYAFLKTYNSLGADLTPFGQELVNS 121

Db	80	SRHGARYPTDSKGKYSALIEIQONATTFDGKYAFKTYNYSLGADLLTFPGEQELVNS	139	CC	to inositol and inorganic phosphate. It shows optimum activity at pH 5.5
Qy	122	GKIFQRYESLTRNIVPTIRSGSRVIAAGKFFIEGFQSTKLKDPRAQPGQSSPKIDW	181	CC	and 2.5, has a specific activity of about 100 U/mg and a mol.wt. of 85
Db	140	GKIFQRYESLTRNIVPTIRSGSRVIAAGKFFIEGFQSTKLKDPRAQPGQSSPKIDW	199	CC	kDa (56.5 kDa unglycosylated). Its amino acid sequence was deduced from
Qy	182	ISEASSSNTLDPGCTVFEDSELADTVANFTATFVPSIRORLENDLSGVTLTTEVTY	241	CC	an isolated phytase cDNA clone (AAT65136). Isolation of this clone allows
Db	200	ISEASSSNTLDPGCTVFEDSELADTVANFTATFVPSIRORLENDLSGVTLTTEVTY	259	CC	large-scale prodn. of the phytase in transformed host cells and used to
Qy	242	LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDLSKLYKHGAGNPLGPTQGVY	301	CC	prepare animal feed, reduce phytase levels in manure (by adding the
Db	260	LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDLSKLYKHGAGNPLGPTQGVY	319	CC	enzyme to animal feed), and also to liberate inorganic phosphates from
Qy	302	ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGIISILFALGLYNGTK	361	CC	myoinositol phosphates in e.g. starch prodn. from cereals and soy
Db	320	ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGIISILFALGLYNGTK	379	CC	processing. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-
Qy	362	PLSTTTVENITQTDGFSSAWTPFASRLYVEMMQCAEQEPLVRLVNDVRVPLHGCPVD	421	CC	MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
Db	380	PLSTTTVENITQTDGFSSAWTPFASRLYVEMMQCAEQEPLVRLVNDVRVPLHGCPVD	439	CC	field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 17-OCT-
Qy	422	ALGRCRTRDSFVRGLSFARSGGDWAECEFA	449	CC	2003 to standardise OS field)
Db	440	ALGRCRTRDSFVRGLSFARSGGDWAECEFA	467	XX	Sequence 467 AA;
RESULT 5					
AAW15124					Query Match 99.8%; Score 2353; DB 2; Length 467;
ID	AAW15124	standard; protein; 467 AA.			Best Local Similarity 100.0%; Pred. No. 1.8e-215;
XX	AAW15124;				Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	17-OCT-2003 (revised)				
DT	25-MAR-2003 (revised)				
DT	21-AUG-1997 (first entry)				
XX	Aspergillus ficum phytase.				
XX	Phytase; phytate; inositol; animal feed.				
XX	Aspergillus ficum; NRRL 3135.				
XX	Key Location/Qualifiers				
XX	Peptide 1..23				
XX	/label= Sig_peptide				
XX	EP779037-A1.				
XX	18-JUN-1997.				
XX	27-SEP-1990; 96EP-00202943.				
XX	27-SEP-1989; 89EP-00202436.				
XX	17-AUG-1990; 90EP-00202231.				
XX	27-SEP-1990; 90EP-00202565.				
XX	(KONN) GIST-BROCADES NV.				
XX	(STAM) DSM NV.				
XX	Van Paridon PA, Veenstra AE, Luiten RGM, Selden GCM;				
XX	Van Gorcom RFM, van Hartingsveldt W;				
XX	WPI; 1997-312513/29.				
XX	N-PSDB; AAT65136, AAT65137.				
XX	Fungal phytase - releases inorganic phosphate from myoinositol phosphate,				
XX	useful to prepare animal feed and reduce phytate levels in manure.				
XX	Example 8; Fig 8; 61pp; English.				
XX	Aspergillus ficum phytase (AAW15124) catalyses the conversion of phytate				

CC	to inositol and inorganic phosphate. It shows optimum activity at pH 5.5
CC	and 2.5, has a specific activity of about 100 U/mg and a mol.wt. of 85
CC	kDa (56.5 kDa unglycosylated). Its amino acid sequence was deduced from
CC	an isolated phytase cDNA clone (AAT65136). Isolation of this clone allows
CC	large-scale prodn. of the phytase in transformed host cells and used to
CC	prepare animal feed, reduce phytase levels in manure (by adding the
CC	enzyme to animal feed), and also to liberate inorganic phosphates from
CC	myoinositol phosphates in e.g. starch prodn. from cereals and soy
CC	processing. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-
CC	MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
CC	field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 17-OCT-
XX	2003 to standardise OS field)
SQ	Sequence 467 AA;
Query Match	99.8%; Score 2353; DB 2; Length 467;
Best Local Similarity	100.0%; Pred. No. 1.8e-215;
Matches 448; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	2 LAVPASRNQSSCDTVDQGYCFSETSHLMGWQYAPFSLANESVISEVPAGCRVTPAQVL 61
Db	20 LAVPASRNQSSCDTVDQGYCFSETSHLMGWQYAPFSLANESVISEVPAGCRVTPAQVL 79
Qy	62 SRHGARYPTDSKGKYSALIEIQONATTFDGKYAFKTYNYSLGADLLTFPGEQELVNS 121
Db	80 SRHGARYPTDSKGKYSALIEIQONATTFDGKYAFKTYNYSLGADLLTFPGEQELVNS 139
Qy	122 GKIFQRYESLTRNIVPTIRSGSRVIAAGKFFIEGFQSTKLKDPRAQPGQSSPKIDVV 181
Db	140 GKIFQRYESLTRNIVPTIRSGSRVIAAGKFFIEGFQSTKLKDPRAQPGQSSPKIDVV 199
Qy	182 ISEASSSNTLDPGCTVFEDSELADTVANFTATFVPSIRORLENDLSGVTLTTEVTY 241
Db	200 ISEASSSNTLDPGCTVFEDSELADTVANFTATFVPSIRORLENDLSGVTLTTEVTY 259
Qy	242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDLSKLYKHGAGNPLGPTQGVY 301
Db	260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDLSKLYKHGAGNPLGPTQGVY 319
Qy	302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db	320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy	362 PLSTTTVENITQTDGFSSAWTPFASRLYVEMMQCAEQEPLVRLVNDVRVPLHGCPVD 421
Db	380 PLSTTTVENITQTDGFSSAWTPFASRLYVEMMQCAEQEPLVRLVNDVRVPLHGCPVD 439
Qy	422 ALGRCRTRDSFVRGLSFARSGGDWAECEFA 449
Db	440 ALGRCRTRDSFVRGLSFARSGGDWAECEFA 467
RESULT 6	
AAAY39904	
ID	AAAY39904 standard; protein; 467 AA.
XX	AAAY39904;
XX	07-DEC-1999 (first entry)
XX	A. ficum phytase protein sequence.
XX	Phytase; variant; enzyme; phosphorus liberation; phytase substrate;
XX	phytate level reduction; animal manure; food preparation; soy processing;
XX	inositol manufacture.
XX	Aspergillus ficum.
XX	WO9949022-A1.
XX	30-SEP-1999.
XX	22-MAR-1999; 99WO-DK000153.

XX 23-MAR-1998; 98DK-00000407.
 PR 19-JUN-1998; 98DK-00000806.
 PR 18-SEP-1998; 98DK-00001176.
 PR 22-JAN-1999; 99DK-00000091.
 XX (NOVO) NOVO-NORDISK AS.
 XX PA
 XX SVENDSEN A;
 XX PI
 XX WPI; 1999-580444/49.
 DR N-PSDB; AA27421.
 XX New variant phytase enzymes, used for liberating phosphorus from a
 PT Phytase substrate, for reducing phytate levels in animal manure and in
 PT feed and food preparations.
 XX
 XX Claim 19; Fig 11; 141pp; English.
 XX PS
 XX This sequence represents the Aspergillus ficum phytase sequence. The
 CC invention relates to variant phytase enzymes with specific amino acid
 CC substitutions for improved properties. The phytase variants can be used
 CC for liberating phosphorus from a phytase substrate. They can be used for
 CC reducing phytate levels in animal manure. They can be used in feed or
 CC food preparations. The phytase DNA can also be used to produce transgenic
 CC plants which can be used in feeds or foods. The phytase variants can also
 CC be used in soy processing and in the manufacture of inositol or
 CC derivatives. The phytase variants can have altered activities such as pH
 CC stability, temperature stability, pH profile, temperature profile,
 CC specific activity (in particular in relation to pH and temperature),
 CC substrate specificity, substrate cleavage pattern, substrate binding,
 CC position specificity, the velocity and level of release of phosphate from
 CC corn, reaction rate, phytase degradation rate and end level of released
 CC phosphate reached
 XX
 XX Sequence 467 AA;
 SQ
 Query Match 99.8%; Score 2353; DB 2; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.8e-215;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LAVPASRNQSSCDTVDQYQCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTFQAQVL 61
 DB 20 LAVPASRNQSSCDTVDQYQCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTFQAQVL 79
 QY 62 SRHGARYPTDSKGKYSALIEIQONATTFDGKXAFKTYNYSIGADDLTFPGEQELVNS 121
 DB 80 SRHGARYPTDSKGKYSALIEIQONATTFDGKXAFKTYNYSIGADDLTFPGEQELVNS 139
 QY 122 GIKFYQRYESLTRNIVPPIRSSGSSRVIASGKFFIEGFQSTKLKDPRAQPGQSSPKIDVV 181
 DB 140 GIKFYQRYESLTRNIVPPIRSSGSSRVIASGKFFIEGFQSTKLKDPRAQPGQSSPKIDVV 199
 QY 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDEVTY 241
 DB 200 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDEVTY 259
 QY 242 LMDMCSFDTISTSTVDTKLSFCDLFDHDEWINDYQLSKKYYGHGAGNPLGPTQGVGY 301
 DB 260 LMDMCSFDTISTSTVDTKLSFCDLFDHDEWINDYQLSKKYYGHGAGNPLGPTQGVGY 319
 QY 302 ANELIARLTHSPVHDDTSSNHTLSSPATPPLNSTLYADFSDHNGIISILFALGLYNGTK 361
 DB 320 ANELIARLTHSPVHDDTSSNHTLSSPATPPLNSTLYADFSDHNGIISILFALGLYNGTK 379
 QY 362 PLSTTTVENTITQDGFSSANTVPASRLYVEMMQCAEQEPLVRVLVNDVRVPLHGCPVD 421
 DB 380 PLSTTTVENTITQDGFSSANTVPASRLYVEMMQCAEQEPLVRVLVNDVRVPLHGCPVD 439
 QY 422 ALGRCRDSFVRGLSFARSGGDWAECEFA 449
 DB 440 ALGRCRDSFVRGLSFARSGGDWAECEFA 467

RESULT 7
 AB83810
 ID AB83810 standard; protein; 467 AA.
 XX AC
 XX ABB83810;
 XX 17-SEP-2002 (first entry)
 DE Aspergillus niger phyA related polypeptide 1.
 XX Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; enzyme.
 XX Aspergillus niger.
 PN CN1333363-A.
 XX 30-JAN-2002.
 XX 12-JUL-2000; 2000CN-00117245.
 XX 12-JUL-2000; 2000CN-00117245.
 XX (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.
 XX Chen Z, Yang L, Fang L;
 DR WPI; 2002-305615/35.
 DR N-PSDB; ABN85588.
 XX Phytase gene sequence and application in yeast thereof.
 XX Disclosure; Fig 2; 48pp; Chinese.
 CC The invention relates to a coded phytase gene sequence suitable for
 CC secretion and expression in yeast and its application. It is mainly
 CC characterised by removing nucleotide sequence of +45-+146 bit from phyA
 CC total length structure gene sequence, removing Aspergillus niger signal
 CC peptide coded sequence of +1-+44 and +147-+159, connecting a part of
 CC signal peptide code sequence suitable for secretion and expression at 5'
 CC end and connecting a restriction endonuclease site at 3' end. The
 CC different carriers can be connected into said gene sequence so as to form
 CC a recombinant plasmid with different functions and after the recombinant
 CC plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
 CC yeast, finally the invented Pasteur Pichia yeast engineering bacterium
 CC (CCTCC NO:M200005) can be obtained through the screening process. By
 CC using the invention the industrial process of phytase bio-expression can
 CC be successfully implemented. The present sequence is that of a
 CC polypeptide of the invention
 XX Sequence 467 AA;
 SQ
 Query Match 99.8%; Score 2353; DB 5; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.8e-215;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LAVPASRNQSSCDTVDQYQCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTFQAQVL 61
 DB 20 LAVPASRNQSSCDTVDQYQCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTFQAQVL 79
 QY 62 SRHGARYPTDSKGKYSALIEIQONATTFDGKXAFKTYNYSIGADDLTFPGEQELVNS 121
 DB 80 SRHGARYPTDSKGKYSALIEIQONATTFDGKXAFKTYNYSIGADDLTFPGEQELVNS 139
 QY 122 GIKFYQRYESLTRNIVPPIRSSGSSRVIASGKFFIEGFQSTKLKDPRAQPGQSSPKIDVV 181
 DB 140 GIKFYQRYESLTRNIVPPIRSSGSSRVIASGKFFIEGFQSTKLKDPRAQPGQSSPKIDVV 199
 QY 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDEVTY 241
 DB 200 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDEVTY 259
 QY 242 LMDMCSFDTISTSTVDTKLSFCDLFDHDEWINDYQLSKKYYGHGAGNPLGPTQGVGY 301

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Db 260 LMDMCSFDTISTVDTKLSPPCDLFTDHEWNIYDLSLKKYHGHGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGHIIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGHIIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQDGFSSAWTPPFASRLYVEMWQCAEQEPLVRVLVNDVRVPLHGCPCVD 421
Db 380 PLSTTTVENITQDGFSSAWTPPFASRLYVEMWQCAEQEPLVRVLVNDVRVPLHGCPCVD 439
QY 422 ALGRCRTRDSFVRLGSLFARSGGDWAECA 449
Db 440 ALGRCRTRDSFVRLGSLFARSGGDWAECA 467

RESULT 8
ADL91242
ID ADL91242 standard; protein; 467 AA.
XX AC ADL91242;
DT 17-JUN-2004 (first entry)
XX DE Wild-type phytase, SEQ ID 2.
XX KW Phytase; enzyme; foodstuff; animal feed; inositol phosphate.
XX OS Aspergillus niger.
XX FN WO2004024885-A2.
XX PD 25-MAR-2004.
XX PE 15-SEP-2003; 2003WO-US028923.
XX PR 13-SEP-2002; 2002US-0410736P.
XX PA (CORR) CORNELL RES FOUND INC.
XX PA (USDA) US SEC OF AGRIC.
XX PI Lei X, Mullaney EJ, Ullah AHJ;
XX WPI; 2004-270029/25.
XX DR N-PSDB; ADL91241.
XX PT Novel isolated mutant phytase e.g. PhyA useful for feeding monogastric
XX PT animals, improving nutritional value of foodstuffs consumed by animal, in
XX PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
XX PT consumed by humans.
XX PS Example 1; SEQ ID NO 2; 215pp; English.
XX CC The present invention relates to mutant phytases (I) and their coding
XX CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
XX CC (I) have altered pH profiles and altered pH optima compared to a
XX CC corresponding non-mutant phytase. (I) are useful for improving the
XX CC nutritional value of a foodstuff which involves providing a foodstuff
XX CC comprising myo-inositol hexakisphosphate, providing (I) and feeding to
XX CC the animal the foodstuff in combination with (I) under conditions
XX CC effective to increase the bioavailability of phosphate from phytate. (I)
XX CC are also useful for feeding a monogastric animal (e.g., fowl species,
XX CC porcine species, aquatic species, domestic animal chosen from canine
XX CC species and a feline species, or mammalian species chosen from
XX CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
XX CC foodstuff in combination with (I), to the animal. (I) are also useful for
XX CC producing specific inositol phosphate metabolites or products for
XX CC nutritional and biomedical applications. The present sequence is a wild-
XX CC type phytase, which was used to produce the mutants of the invention.
XX SQ Sequence 467 AA;

Query Match 99.8%; Score 2353; DB 8; Length 467;

Best Local Similarity 100.0%; Pred. No. 1.8e-215; Indels 0; Gaps 0;
Matches 448; Conservative 0; Mismatches 0;
QY 2 LAVPASRNOSSCDTVDQGYQCFSETSHLWGVAPFPFSLANESVISPVEPAGCRVTFQAQVL 61
Db 20 LAVPASRNOSSCDTVDQGYQCFSETSHLWGVAPFPFSLANESVISPVEPAGCRVTFQAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEEIQONATTFDGYAFPLKTYNYSGLGADDLTPFGEOELVNS 121
Db 80 SRHGARYPTDSKGGKYSALIEEIQONATTFDGYAFPLKTYNYSGLGADDLTPFGEOELVNS 139
QY 122 GIKFYQRYESLTRNIVPPIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGOSSPKIDVV 181
Db 140 GIKFYQRYESLTRNIVPPIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGOSSPKIDVV 199
QY 182 ISEASSNNLDPGCTVTFEDSELADTVEANFTAFVPSIRORLENDLSGVTITDTEVTY 241
Db 200 ISEASSNNLDPGCTVTFEDSELADTVEANFTAFVPSIRORLENDLSGVTITDTEVTY 259
QY 242 LMDMCSFDTISTVDTKLSPPCDLFTDHEWNIYDLSLKKYHGHGAGNPLGPTQGVY 301
Db 260 LMDMCSFDTISTVDTKLSPPCDLFTDHEWNIYDLSLKKYHGHGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGHIIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGHIIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQDGFSSAWTPPFASRLYVEMWQCAEQEPLVRVLVNDVRVPLHGCPCVD 421
Db 380 PLSTTTVENITQDGFSSAWTPPFASRLYVEMWQCAEQEPLVRVLVNDVRVPLHGCPCVD 439
QY 422 ALGRCRTRDSFVRLGSLFARSGGDWAECA 449
Db 440 ALGRCRTRDSFVRLGSLFARSGGDWAECA 467

RESULT 9
ADL91268
ID ADL91268 standard; protein; 467 AA.
XX AC ADL91268;
XX DT 17-JUN-2004 (first entry)
XX DE Mutant phytase, K300R, SEQ ID 28.
XX KW Mutant; mutant; phytase; enzyme; foodstuff; animal feed;
XX KW inositol phosphate.
XX OS Aspergillus niger.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 300 /note= "Wild-type residue replaced with Arg"

WO2004024885-A2.

25-MAR-2004.

15-SEP-2003; 2003WO-US028923.

13-SEP-2002; 2002US-0410736P.

(CORR) CORNELL RES FOUND INC.

(USDA) US SEC OF AGRIC.

Lei X, Mullaney EJ, Ullah AHJ;

WPI; 2004-270029/25.

DR N-PSDB; ADL91267.

Novel isolated mutant phytase e.g. PhyA useful for feeding monogastric

PT animals, improving nutritional value of foodstuffs consumed by animal, in
 PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
 consumed by humans.

XX Claim 40; SEQ ID NO 28; 215pp; English.

XX The present invention relates to mutant phytases (I) and their coding
 CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
 CC (I) have altered pH profiles and altered pH optima compared to a
 CC corresponding non-mutant phytase. (I) are useful for improving the
 CC nutritional value of a foodstuff which involves providing a foodstuff
 CC comprising myo-inositol hexakisphosphate, providing (I) and feeding to
 CC the animal the foodstuff in combination with (I) under conditions
 CC effective to increase the bioavailability of phosphate from phytate. (I)
 CC are also useful for feeding a monogastric animal (e.g., fowl species,
 CC porcine species, aquatic species, domestic animal chosen from canine
 CC species and a feline species, or mammalian species chosen from
 CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
 CC foodstuff in combination with (I), to the animal. (I) are also useful for
 CC producing specific inositol phosphate metabolites or products for
 CC nutritional and biomedical applications. The present sequence is one such
 CC mutant phytase.

XX Sequence 467 AA;

Query Match 99.7%; Score 2350; DB 8; Length 467;

Best Local Similarity 99.8%; Pred. No. 3.5e-215;
 Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSESHLWGQYAPFSLANESVISEVPAGCRVTFQAQL 61

DB 20 LAVPASRNQSSCDTVDQGYQCFSESHLWGQYAPFSLANESVISEVPAGCRVTFQAQL 79

QY 62 SRHGARYPTDSKGYKYSALIEIQONATTFDGKFAFLKTYNSLGGADLTTPGQELVNS 121

DB 80 SRHGARYPTDSKGYKYSALIEIQONATTFDGKFAFLKTYNSLGGADLTTPGQELVNS 139

QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDPRAQPGQSSPKIDV 181

DB 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDPRAQPGQSSPKIDV 199

QY 182 ISEASSNNTLDPGCTVFEDELADTVEANFTATFVPSIRQLENLSGVTLTDEVY 241

DB 200 ISEASSNNTLDPGCTVFEDELADTVEANFTATFVPSIRQLENLSGVTLTDEVY 259

QY 242 LMDMCSFTTISTVDTKLSPFCDLFTHDEWINYDLSLKYKHGAGNPLGPTQGVY 301

DB 260 LMDMCSFTTISTVDTKLSPFCDLFTHDEWINYDLSLKYKHGAGNPLGPTQGVY 319

QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPINSTLYADFSDNGIISILFALGLYNGTK 361

DB 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPINSTLYADFSDNGIISILFALGLYNGTK 379

QY 362 PLSTTTVNITQTDFSSAWTVPPASRLYVENMQCAEQEPLRVLRVNDVRVPLHGCPVD 421

DB 380 PLSTTTVNITQTDFSSAWTVPPASRLYVENMQCAEQEPLRVLRVNDVRVPLHGCPVD 439

QY 422 ALGRCTRDSFVRGLSFARSGGDWAECA 449

DB 440 ALGRCTRDSFVRGLSFARSGGDWAECA 467

RESULT 10

ADL91262

XX ADL91262 standard; protein; 467 AA.

XX AC ADL91262;

XX 17-JUN-2004 (first entry)

DT Mutant phytase, E228Q, SEQ ID 22.

XX Mutant; mutein; phytase; enzyme; foodstuff; animal feed;

XX

KW inositol phosphate.
 XX Aspergillus niger.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 228 /note= "Wild-type residue replaced with Gln"
 XX

PN W02004024885-A2.

XX 25-MAR-2004.

XX 15-SEP-2003; 2003WO-US028923.

XX 13-SEP-2002; 2002US-0410736P.

XX (CORR) CORNELL RES FOUND INC.

XX (USDA) US SEC OF AGRIC.

XX Lei X, Mullaney EJ, Ullah AHJ;

XX WPI; 2004-270029/25.

XX N-PSDB; ADL91261.

XX Novel isolated mutant phytase e.g. Phya useful for feeding monogastric
 PT animals, improving nutritional value of foodstuffs consumed by animal, in
 PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
 consumed by humans.

XX Claim 38; SEQ ID NO 22; 215pp; English.

XX The present invention relates to mutant phytases (I) and their coding
 CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
 CC (I) have altered pH profiles and altered pH optima compared to a
 CC corresponding non-mutant phytase. (I) are useful for improving the
 CC nutritional value of a foodstuff which involves providing a foodstuff
 CC comprising myo-inositol hexakisphosphate, providing (I) and feeding to
 CC the animal the foodstuff in combination with (I) under conditions
 CC effective to increase the bioavailability of phosphate from phytate. (I)
 CC are also useful for feeding a monogastric animal (e.g., fowl species,
 CC porcine species, aquatic species, domestic animal chosen from canine
 CC species and a feline species, or mammalian species chosen from
 CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
 CC foodstuff in combination with (I), to the animal. (I) are also useful for
 CC producing specific inositol phosphate metabolites or products for
 CC nutritional and biomedical applications. The present sequence is one such
 CC mutant phytase.

XX Sequence 467 AA;

Query Match 99.7%; Score 2350; DB 8; Length 467;

Best Local Similarity 99.8%; Pred. No. 3.5e-215;
 Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSESHLWGQYAPFSLANESVISEVPAGCRVTFQAQL 61

DB 20 LAVPASRNQSSCDTVDQGYQCFSESHLWGQYAPFSLANESVISEVPAGCRVTFQAQL 79

QY 62 SRHGARYPTDSKGYKYSALIEIQONATTFDGKFAFLKTYNSLGGADLTTPGQELVNS 121

DB 80 SRHGARYPTDSKGYKYSALIEIQONATTFDGKFAFLKTYNSLGGADLTTPGQELVNS 139

QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDPRAQPGQSSPKIDV 181

DB 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDPRAQPGQSSPKIDV 199

QY 182 ISEASSNNTLDPGCTVFEDELADTVEANFTATFVPSIRQLENLSGVTLTDEVY 241

DB 200 ISEASSNNTLDPGCTVFEDELADTVEANFTATFVPSIRQLENLSGVTLTDEVY 259

QY 242 LMDMCSFTTISTVDTKLSPFCDLFTHDEWINYDLSLKYKHGAGNPLGPTQGVY 301

CC	mutant	phytase.
XX	Sequence	467 AA;
XX	Query Match	99.6%; Score 2349; DB 8; Length 467;
XX	Best Local Similarity	99.8%; Pred. No. 4.4e-215;
XX	Matches	447; Conservative
QY	2	LAVPASRNOSCDTVDOGYQCFSETSHLWGOYAPFFSLANESVISPEVPAGCRVTTFAQVL 61
Db	20	LAVPASRNOSCDTVDOGYQCFSETSHLWGOYAPFFSLANESVISPEVPAGCRVTTFAQVL 79
QY	62	SRHGARYPTDSKGKYSALIEEIQONATTFDGKYAFLLKTYNSLGADLLTPFGQELVNS 121
Db	80	SRHGARYPTDSKGKYSALIEEIQONATTFDGKYAFLLKTYNSLGADLLTPFGQELVNS 139
QY	122	GKIFYORYESLIRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVV 181
Db	140	GKIFYORYESLIRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVV 199
QY	182	ISRASNNNTLDPGTCVFPEDSELADTVEANFTATFVPSIRQRLNDLSGVTLLDTTEVY 241
Db	200	ISRASNNNTLDPGTCVFPEDSELADTVEANFTATFVPSIRQRLNDLSGVTLLDTTEVY 259
QY	242	LMDMCSFDTTSTVTDTKLSPFCDLFTHDEWINVDYLOSLKKYXCHGAGNPLGPTQGQVGY 301
Db	260	LMDMCSFDTTSTVTDTKLSPFCDLFTHDEWINVDYLOSLKKYXCHGAGNPLGPTQGQVGY 319
QY	302	ANELIARLTHSPVHDDTSSNHTLDS SPATPLNSTLYADFSDHNGIISILFALGLYNGTK 361
Db	320	ANELIARLTHSPVHDDTSSNHTLDS SPATPLNSTLYADFSDHNGIISILFALGLYNGTK 379
QY	362	PLSTTTVENITQTDGFSASATVPFASKLYVEMMOCQAEQEPPLRVLVNDRVVPPLHGCPVD 421
Db	380	PLSTTTVENITQTDGFSASATVPFASKLYVEMMOCQAEQEPPLRVLVNDRVVPPLHGCPVD 439
QY	422	ALGCTRDTSFVRGLSPARSGGDWAECEFA 449
Db	440	ALGCTRDTSFVRGLSPARSGGDWAECEFA 467
RESULT	12	
ADL91264	ID	ADL91264 standard; protein; 467 AA.
XX	AC	ADL91264;
XX	DT	17-JUN-2004 (first entry)
XX	DE	Mutant phytase, E228K, SEQ ID 24.
XX	KW	Mutant; mutein; phytase; enzyme; foodstuff; animal feed;
XX	KW	inositol phosphate.
XX	OS	Aspergillus niger.
XX	OS	Synthetic.
XX	FH	Key
XX	FT	Misc-difference 228
XX	FT	/note= "Wild-type residue replaced with Lys"
XX	PN	WO2004024885-A2.
XX	XX	25-MAR-2004.
XX	XX	15-SEP-2003; 2003WO-US028923.
XX	XX	13-SEP-2002; 2002US-0410736P.
XX	XX	(CORR) CORNELL RES FOUND INC.
XX	PA	(USDA) US SEC OF AGRIC.
XX	PI	Lei X, Mullaney EJ, Ullah AHJ;

XX WPI; 2004-270029/25.
 DR N-PSDB; ADL91263.
 XX
 PT Novel isolated mutant phytase e.g. Phya useful for feeding monogastric
 PT animals, improving nutritional value of foodstuffs consumed by animal, in
 PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
 PT consumed by humans.
 XX
 PS Claim 38; SEQ ID NO 24; 215pp; English.
 XX
 CC The present invention relates to mutant phytases (I) and their coding
 CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
 CC (I) have altered pH profiles and altered pH optima compared to a
 CC corresponding non-mutant phytase. (I) are useful for improving the
 CC nutritional value of a foodstuff which involves providing a foodstuff
 CC comprising myo-inositol hexakisphosphate, providing (I) and feedings to
 CC the animal the foodstuff in combination with (I) under conditions
 CC effective to increase the bioavailability of phosphate from phytate. (I)
 CC are also useful for feeding a monogastric animal (e.g., fowl species,
 CC porcine species, aquatic species, domestic animal chosen from canine
 CC species and a feline species, or mammalian species chosen from
 CC Cryptolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
 CC foodstuff in combination with (I), to the animal. (I) are also useful for
 CC producing specific inositol phosphate metabolites or products for
 CC nutritional and biomedical applications. The present sequence is one such
 CC mutant phytase.
 XX
 SQ Sequence 467 AA;
 Query Match 99.6%; Score 2349; DB 8; Length 467;
 Best Local Similarity 99.8%; Pred. No. 4.4e-215;
 Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LAVPASRNSQSCDVTVDGQYQCFSTSHLWQYAPFFSLANESVISPVPAGCRVTFPAQVL 61
 DB 20 LAVPASRNSQSCDVTVDGQYQCFSTSHLWQYAPFFSLANESVISPVPAGCRVTFPAQVL 79
 QY 62 SRHGARYPTDSKGKYSALIEIQONATTFDGKVAFLKTYNSIGADDLTPFGQELVNS 121
 DB 80 SRHGARYPTDSKGKYSALIEIQONATTFDGKVAFLKTYNSIGADDLTPFGQELVNS 139
 QY 122 GIKFYQYVESLTRNIVPFISSGSSSRVSIASGKKEIEGFQSTKLDPRAQPGQSSPKIDVV 181
 DB 140 GIKFYQYVESLTRNIVPFISSGSSSRVSIASGKKEIEGFQSTKLDPRAQPGQSSPKIDVV 199
 QY 182 ISEASSNNLDPGTCVTFEDSELADTVKANFTATFVPSIRQRLNLSGVTLTDTEVTY 241
 DB 200 ISEASSNNLDPGTCVTFEDSELADTVKANFTATFVPSIRQRLNLSGVTLTDTEVTY 259
 QY 242 LMDMCSFDTTSTVDTKLSPFCDLFTHDEWINDYLSLKKYGHGAGNPLGPTQGVY 301
 DB 260 LMDMCSFDTTSTVDTKLSPFCDLFTHDEWINDYLSLKKYGHGAGNPLGPTQGVY 319
 QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPINSTLYADFSDHNGIISILFALGLYNGTK 361
 DB 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPINSTLYADFSDHNGIISILFALGLYNGTK 379
 QY 362 PLSTTTVENTITQDGFSAWTVPPASRLYVEMMQCAEQEPLVRLVNDVRVPLHGCPVD 421
 DB 380 PLSTTTVENTITQDGFSAWTVPPASRLYVEMMQCAEQEPLVRLVNDVRVPLHGCPVD 439
 QY 422 ALGRCTRDSFVRGLSFARSGGDWAECEA 449
 DB 440 ALGRCTRDSFVRGLSFARSGGDWAECEA 467
 RESULT 13
 ID ADL91274
 ID ADL91274 standard; protein; 467 AA.
 XX
 AC ADL91274;
 XX

DT 17-JUN-2004 (first entry)
 XX
 DE Mutant phytase, K301E, SEQ ID 34.
 XX
 KW Mutant; mutein; phytase; enzyme; foodstuff; animal feed;
 KW inositol phosphate.
 OS Aspergillus niger.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 301
 FT /note= "Wild-type residue replaced with Glu"
 FN WO2004024885-A2.
 PD 25-MAR-2004.
 XX
 FF 15-SEP-2003; 2003WO-US028923.
 XX
 FF 13-SEP-2002; 2002US-0410736P.
 PR (CORR) CORNELL RES FOUND INC.
 PA (USDA) US SEC OF AGRIC.
 XX
 PI Lei X, Mullaney EJ, Ullah AHJ;
 XX
 DR WPI; 2004-270029/25.
 DR N-PSDB; ADL91273.
 XX
 PT Novel isolated mutant phytase e.g. Phya useful for feeding monogastric
 PT animals, improving nutritional value of foodstuffs consumed by animal, in
 PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
 PT consumed by humans.
 XX
 PS Claim 41; SEQ ID NO 34; 215pp; English.
 XX
 CC The present invention relates to mutant phytases (I) and their coding
 CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
 CC (I) have altered pH profiles and altered pH optima compared to a
 CC corresponding non-mutant phytase. (I) are useful for improving the
 CC nutritional value of a foodstuff which involves providing a foodstuff
 CC comprising myo-inositol hexakisphosphate, providing (I) and feedings to
 CC the animal the foodstuff in combination with (I) under conditions
 CC effective to increase the bioavailability of phosphate from phytate. (I)
 CC are also useful for feeding a monogastric animal (e.g., fowl species,
 CC porcine species, aquatic species, domestic animal chosen from canine
 CC species and a feline species, or mammalian species chosen from
 CC Cryptolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
 CC foodstuff in combination with (I), to the animal. (I) are also useful for
 CC producing specific inositol phosphate metabolites or products for
 CC nutritional and biomedical applications. The present sequence is one such
 CC mutant phytase.
 XX
 SQ Sequence 467 AA;
 Query Match 99.6%; Score 2349; DB 8; Length 467;
 Best Local Similarity 99.8%; Pred. No. 4.4e-215;
 Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LAVPASRNSQSCDVTVDGQYQCFSTSHLWQYAPFFSLANESVISPVPAGCRVTFPAQVL 61
 DB 20 LAVPASRNSQSCDVTVDGQYQCFSTSHLWQYAPFFSLANESVISPVPAGCRVTFPAQVL 79
 QY 62 SRHGARYPTDSKGKYSALIEIQONATTFDGKVAFLKTYNSIGADDLTPFGQELVNS 121
 DB 80 SRHGARYPTDSKGKYSALIEIQONATTFDGKVAFLKTYNSIGADDLTPFGQELVNS 139
 QY 122 GIKFYQYVESLTRNIVPFISSGSSSRVSIASGKKEIEGFQSTKLDPRAQPGQSSPKIDVV 181
 DB 140 GIKFYQYVESLTRNIVPFISSGSSSRVSIASGKKEIEGFQSTKLDPRAQPGQSSPKIDVV 199
 QY 182 ISEASSNNLDPGTCVTFEDSELADTVKANFTATFVPSIRQRLNLSGVTLTDTEVTY 241

||||| 200 ISEASSNNLTDPGCTVFEDSELADTVEANFTATVPISIRQLENDLSGVTLTDEVTY 259
Db
||||| 242 LMDMCSFDITSTVDTKLSPPCDLFTHDEWINYDLSKKYHGAGNPLGPTQGVY 301
Qy
||||| 260 LMDMCSFDITSTVDTKLSPPCDLFTHDEWINYDLSKKYHGAGNPLGPTQGVY 319
Db
||||| 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Qy
||||| 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Db
||||| 362 PLSTTTVENITQDGFSSAWTVPFASRLYVENMQCAEQEPLVRVLVNDVRVPLHGCPVD 421
Qy
||||| 380 PLSTTTVENITQDGFSSAWTVPFASRLYVENMQCAEQEPLVRVLVNDVRVPLHGCPVD 439
Db
||||| 422 ALGRCTRDSFVRGLSFARSGGDWAECEFA 449
Qy
||||| 440 ALGRCTRDSFVRGLSFARSGGDWAECEFA 467
Db

RESULT 14
ADL91248
ID ADL91248 standard; protein; 467 AA.
XX
AC ADL91248;
XX
DT 17-JUN-2004 (first entry)
XX
DE Mutant phytase, K300E, SEQ ID 8.
XX
KW Mutant; mutein; phytase; enzyme; foodstuff; animal feed;
KW inositol phosphate.
XX
OS Aspergillus niger.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 300 /note= "wild-type residue replaced with Glu"
FT
XX
XX WO2004024885-A2.
XX
XX 25-MAR-2004.
XX
XX 15-SEP-2003; 2003WO-US028923.
XX
XX 13-SEP-2002; 2002US-0410736P.
XX
XX (CORR) CORNELL RES FOUND INC.
XX (USDA) US SEC OF AGRIC.
XX
XX Lei X, Mullaney BJ, Ullah AHJ;
XX
XX WPI; 2004-270029/25.
XX N-PSDB; ADL91247.
XX
XX Novel isolated mutant phytase e.g. PhvA useful for feeding monogastric
PT animals, improving nutritional value of foodstuffs consumed by animal, in
PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
PT consumed by humans.
XX
XX Claim 40; SEQ ID NO 8; 215pp; English.
XX
XX The present invention relates to mutant phytases (I) and their coding
CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
CC (I) have altered pH profiles and altered pH optima compared to a
CC corresponding non-mutant phytase. (I) are useful for improving the
CC nutritional value of a foodstuff which involves providing a foodstuff
CC comprising myo-inositol hexakisphosphate, providing (I) and feeding to
CC the animal the foodstuff in combination with (I) under conditions
CC effective to increase the bioavailability of phosphate from phytate. (I)
CC are also useful for feeding a monogastric animal (e.g., fowl species,
CC porcine species, aquatic species, domestic animal chosen from canine

CC species and a feline species, or mammalian species chosen from
CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
CC foodstuff in combination with (I) to the animal. (I) are also useful for
CC producing specific inositol phosphate metabolites or products for
CC nutritional and biomedical applications. The present sequence is one such
CC mutant phytase.
XX
SQ Sequence 467 AA;

Query Match 99.6%; Score 2349; DB 8; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.4e-215;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQVL 79
Qy 62 SRHGARYPTDSKGKYSALIEIQNATTFDGKYAFKTYNYSLGADDLTPFGEQELVNS 121
Db 80 SRHGARYPTDSKGKYSALIEIQNATTFDGKYAFKTYNYSLGADDLTPFGEQELVNS 139
Qy 122 GIKFYQRYESELTRNIVPFRSSGSRVIAASGKKFIEGFQSTKLKOPRAOPGSSPKIDVV 181
Db 140 GIKFYQRYESELTRNIVPFRSSGSRVIAASGKKFIEGFQSTKLKOPRAOPGSSPKIDVV 199
Qy 182 ISEASSNNLTDPGCTVFEDSELADTVEANFTATVPISIRQLENDLSGVTLTDEVTY 241
Db 200 ISEASSNNLTDPGCTVFEDSELADTVEANFTATVPISIRQLENDLSGVTLTDEVTY 259
Qy 242 LMDMCSFDITSTVDTKLSPPCDLFTHDEWINYDLSKKYHGAGNPLGPTQGVY 301
Db 260 LMDMCSFDITSTVDTKLSPPCDLFTHDEWINYDLSKKYHGAGNPLGPTQGVY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQDGFSSAWTVPFASRLYVENMQCAEQEPLVRVLVNDVRVPLHGCPVD 421
Db 380 PLSTTTVENITQDGFSSAWTVPFASRLYVENMQCAEQEPLVRVLVNDVRVPLHGCPVD 439
Qy 422 ALGRCTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGRCTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 15
ADL91258
ID ADL91258 standard; protein; 467 AA.
XX
AC ADL91258;
XX
DT 17-JUN-2004 (first entry)
XX
DE Mutant phytase, K91E, SEQ ID 18.
XX
KW Mutant; mutein; phytase; enzyme; foodstuff; animal feed;
KW inositol phosphate.
XX
OS Aspergillus niger.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 91 /note= "wild-type residue replaced with Glu"
FT
XX
XX WO2004024885-A2.
XX
XX 25-MAR-2004.
XX
XX 15-SEP-2003; 2003WO-US028923.
XX
XX 13-SEP-2002; 2002US-0410736P.

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OM protein - protein search, using sw model

Run on: October 24, 2004, 11:16:03 ; Search time 50 Seconds
(without alignments)
864.027 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MLAVPASRNQSSCDTVDQY.....SFVGLSFARSGDWAECFA 449

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2353	99.8	467	1 JN0656	3-phytase (EC 3.1.1.
2	2315	98.2	441	1 JN0482	3-phytase (EC 3.1.1.
3	2309	97.9	467	1 JN0889	3-phytase (EC 3.1.1.
4	385	16.3	467	1 PABYC	acid phosphatase (
5	385	16.3	467	1 PABYC	acid phosphatase (
6	368	15.6	468	2 S52495	acid phosphatase h
7	352	14.9	467	2 S48996	acid phosphatase (
8	352	14.9	467	2 S53476	acid phosphatase (
9	339.5	14.4	479	1 JN0715	3-phytase (EC 3.1.1.
10	336.5	14.4	479	1 JN0890	acid phosphatase (
11	327	13.9	468	2 JC4285	acid phosphatase (
12	300.5	12.7	453	1 A25326	acid phosphatase (
13	300	12.7	463	2 T39929	thiamin-repressibl
14	284	12.0	463	2 S14119	acid phosphatase (
15	148	6.3	468	2 A86233	hypothetical prote
16	132.5	5.6	465	2 JF0369	histidine acid pho
17	120.5	5.1	413	2 F90773	periplasmic glucos
18	120.5	5.1	413	2 B85636	periplasmic glucos
19	119.5	5.1	413	2 JV0087	glucose-1-phosphat
20	119	5.0	449	2 T15933	hypothetical prote
21	115	4.9	590	2 H70130	oligoendopeptidase
22	114.5	4.9	1756	2 S45867	TyB protein - yeas
23	114	4.8	438	2 S64682	acid phosphatase (
24	111.5	4.7	694	2 I40866	exo-alpha-sialidas
25	111.5	4.7	1032	2 T34433	hypothetical prote
26	111	4.7	1816	2 F82901	hypothetical prote
27	105.5	4.6	553	2 T06179	myb-related protei
28	107	4.5	344	2 H89130	protein F52E1.8 [i
29	107	4.5	1322	2 H86196	hypothetical prote

30	107	4.5	2314	1 A46151	protein-tyrosine-p
31	106.5	4.5	1755	2 S45736	TyB protein - yeas
32	106	4.5	507	1 RNZCV	polymerase-associ
33	106	4.5	755	2 T15118	acid phosphatase h
34	106	4.5	3624	2 AD0835	large repetitive p
35	105.5	4.5	411	2 D88504	protein B0361.7 [i
36	105	4.5	380	2 T16883	hypothetical prote
37	105	4.5	452	2 T20556	hypothetical prote
38	104.5	4.4	1254	2 S46636	hypothetical prote
39	104	4.4	504	2 A25222	MSB2 protein - yea
40	104	4.4	1306	2 S25370	threonine synthase
41	103.5	4.4	470	2 D81353	secreted acid phos
42	103	4.4	537	2 S54770	secreted acid phos
43	103	4.4	888	2 T46726	secreted acid phos
44	102	4.3	927	2 T39127	phosphoprotein - f
45	102	4.3	948	2 T11678	hypothetical prote

ALIGNMENTS

RESULT 1

JN0656

3-phytase (EC 3.1.1.3.8) A precursor - Aspergillus niger

N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein

C:Species: Aspergillus niger

C>Date: 03-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C:Accession: JN0656; S28456

R:van Hartingsveldt, W.; van Zeijl, C.M.J.; Harteveld, G.M.; Gouka, R.J.; Suykerbuyk, M.F. A.M.J.J.

Gene 127, 87-94, 1993

A:Title: Cloning, characterization and overexpression of the phytase-encoding gene (phyA)

A:Reference number: JN0656; MUID:93252284; PMID:8387447

A:Accession: JN0656

A:Molecule type: DNA

A:Residues: 1-467 <V>

A:Cross-references: UNIPROT:P34752; GB:Z16414; NID:g2392; PIDN:CAA78904.1; PID:g2393

A:Experimental source: strain NRRL3135

A:Note: parts of the sequence, including the amino end of the mature protein, were confir

C:Comment: This enzyme catalyzes the hydrolysis of phytic acid into myo-inositol and inos

C:Genetics:

A:Gene: phyA

A:Introns: 15/2

C:Superfamily: yeast acid phosphatase

C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-467/Product: 3-phytase A #status experimental <MAT>

F:27.59,105,120,207,230,339,352,376,388/Binding site: carbohydrate (Asn) (covalent) #stat

F:81,361/Active site: Arg, His #status predicted

F:82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 99.8%; Score 2353; DB 1; Length 467;

Best Local Similarity 100.0%; Pred. No. 6.2e-164;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQYQCFSETSHLWGVAPFFSLANESVLSPEVPACRVTPAQL 61

Db 20 LAVPASRNQSSCDTVDQYQCFSETSHLWGVAPFFSLANESVLSPEVPACRVTPAQL 79

QY 62 SRHGARYPTDSGKKYSALIEIQQNATTFDGKVAFLKTYNYSGLGADDLTFPGEGELVNS 121

Db 80 SRHGARYPTDSGKKYSALIEIQQNATTFDGKVAFLKTYNYSGLGADDLTFPGEGELVNS 139

QY 122 GIKFYQYVESLTRNIVPPIRSGSSSRVTSAGKFTIEGQSTKLKDPRAQPGQSSPKIDW 181

Db 140 GIKFYQYVESLTRNIVPPIRSGSSSRVTSAGKFTIEGQSTKLKDPRAQPGQSSPKIDW 199

QY 182 ISEASSNNTLDPGCTVFEDSELADTVEANFTATFVSIQRLENDLSGYTLTDTFTY 241

Db 200 ISEASSNNTLDPGCTVFEDSELADTVEANFTATFVSIQRLENDLSGYTLTDTFTY 259

QY 242 LMDMCSFTISTSTVDTKLSPFCDLFTHDEWINVDYLSLKKYCHGAGNPLGPTQGVY 301

Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINVDYLQSLKYYVGHGAGNPLGPTQGVY 319
 QY 302 ANELIARLTHSPVHDDTSSNHTLDSSPATFPPLNSTLYADFSHDNGIISILFALGLYNGTK 361
 Db 320 ANELIARLTHSPVHDDTSSNHTLDSSPATFPPLNSTLYADFSHDNGIISILFALGLYNGTK 379
 QY 362 PLSTTTVENTITQTDGSSAWTVFPASRLYYEMMQCAEQEPLVRVLVNDVRVPLHGCPCVD 421
 Db 380 PLSTTTVENTITQTDGSSAWTVFPASRLYYEMMQCAEQEPLVRVLVNDVRVPLHGCPCVD 439
 QY 422 ALGRCRDSFVRGLSFARSGGDWAE 449
 Db 440 ALGRCRDSFVRGLSFARSGGDWAE 467
 RESULT 2
 JN0482
 3-phytase (EC 3.1.3.8) A - Aspergillus ficum
 N;Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phya protein
 C;Species: Aspergillus ficum
 C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
 C;Accession: JN0482; JN0023
 R;Ullah, A.H.J.; Dischinger Jr., H.C.
 Biochem. Biophys. Res. Commun. 192, 747-753, 1993
 A;Title: Aspergillus ficum phytase: Complete primary structure elucidation by chemical
 A;Reference number: JN0482; MUID:93249451; PMID:8387289
 A;Accession: JN0482
 A;Molecule type: protein
 A;Residues: 1-441 <URL>
 A;Cross-references: UNIPROT:P34752
 A;Note: authors state that the 9 Asn followed by Thr or Ser after an intervening residue
 R;Ullah, A.H.J.; Cummins, B.J.; Dischinger Jr., H.C.
 Biochem. Biophys. Res. Commun. 178, 45-53, 1991
 A;Title: Cyclohexanediolone modification of arginine at the active site of Aspergillus fic
 A;Reference number: PN0023; MUID:91298982; PMID:1648914
 A;Accession: PN0023
 A;Molecule type: protein
 A;Residues: 48-70 <URL>
 C;Comment: This enzyme catalyzes the hydrolysis of inorganic orthophosphate from phytate
 C;Superfamily: yeast acid phosphatase
 C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
 F;4,36,82,97,184,207,316,329,353,365/Binding site: carbohydrate (Asn) (covalent) #status
 F;58,338/Active site: Arg, His #status predicted
 F;59/Active site: His (phosphohistidine intermediate) #status predicted
 Query Match 98.2%; Score 2315; DB 1; Length 441;
 Best Local Similarity 100.0%; Pred. No. 3.4e-161;
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ASRNOSSCDTVDOGYQCFSETSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVLSRHG 65
 Db 1 ASRNOSSCDTVDOGYQCFSETSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVLSRHG 60
 QY 66 ARYPYTSKGGKYSALIEEIQNATTFDGKYAFKTYNSLGGADLTTPFGQELVNSGKIF 125
 Db 61 ARYPYTSKGGKYSALIEEIQNATTFDGKYAFKTYNSLGGADLTTPFGQELVNSGKIF 120
 QY 126 YQRYESLTRNIVPPIRSSGSRVITAGKKFIEGQSTKLKDPRAQPGQSSPKIDVISEA 185
 Db 121 YQRYESLTRNIVPPIRSSGSRVITAGKKFIEGQSTKLKDPRAQPGQSSPKIDVISEA 180
 QY 186 SSSNNLTDPGCTVFEDSELADTVANFTAFVPSIRQRLNLSGVTLTDTTEVTYLMDM 245
 Db 181 SSSNNLTDPGCTVFEDSELADTVANFTAFVPSIRQRLNLSGVTLTDTTEVTYLMDM 240
 QY 246 CSFDTISTSTVDTKLSPFCDLFTHDEWINVDYLQSLKYYVGHGAGNPLGPTQGVYANEL 305
 Db 241 CSFDTISTSTVDTKLSPFCDLFTHDEWINVDYLQSLKYYVGHGAGNPLGPTQGVYANEL 300
 QY 306 IARLTHSPVHDDTSSNHTLDSSPATFPPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 365
 Db 301 IARLTHSPVHDDTSSNHTLDSSPATFPPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 360

QY 366 TTVENITQTDGSSAWTVFPASRLYYEMMQCAEQEPLVRVLVNDVRVPLHGCPCVDALGR 425
 Db 361 TTVENITQTDGSSAWTVFPASRLYYEMMQCAEQEPLVRVLVNDVRVPLHGCPCVDALGR 420
 QY 426 CTRDSFVRGLSFARSGGDWAE 446
 Db 421 CTRDSFVRGLSFARSGGDWAE 441
 RESULT 3
 JN0889
 3-phytase (EC 3.1.3.8) A precursor - Aspergillus awamori
 N;Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phya protein
 C;Species: Aspergillus awamori
 C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
 C;Accession: JN0889
 R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; Ne
 Gene 133, 55-62, 1993
 A;Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-optim
 A;Reference number: JN0889; MUID:94040796; PMID:8224894
 A;Accession: JN0889
 A;Molecule type: DNA
 A;Residues: 1-467 <PID>
 A;Cross-references: UNIPROT:P34753; GB:I02421; NID:G166518; PIDN:AAA16898.1; PID:G166519
 A;Experimental source: strain ALK0243
 A;Note: part of the sequence, including the amino end of the mature protein, was confirme
 C;Comment: This enzyme catalyzes the conversion of phytate to inositol and inorganic phos
 C;Genetics:
 A;Gene: phya
 A;Introns: 15/2
 C;Superfamily: yeast acid phosphatase
 C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-467/Product: 3-phytase A #status experimental <MAT>
 F;27,59,105,120,207,230,339,352,376,388/Binding site: carbohydrate (Asn) (covalent) #stat
 F;81,361/Active site: Arg, His #status predicted
 F;82/Active site: His (phosphohistidine intermediate) #status predicted
 Query Match 97.9%; Score 2309; DB 1; Length 467;
 Best Local Similarity 97.3%; Pred. No. 1e-160;
 Matches 436; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 2 LAVPASRNOSSCDTVDOGYQCFSETSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 61
 Db 20 LAVPASRNOSSCDTVDOGYQCFSETSHLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 79
 QY 62 SRHGARYPTDSKGGKYSALIEEIQNATTFDGKYAFKTYNSLGGADLTTPFGQELVNS 121
 Db 80 SRHGARYPTDSKGGKYSALIEEIQNATTFDGKYAFKTYNSLGGADLTTPFGQELVNS 139
 QY 122 GIKFYQRYESLTRNIVPPIRSSGSRVITAGKKFIEGQSTKLKDPRAQPGQSSPKIDVV 181
 Db 140 GIKFYQRYESLTRNIVPPIRSSGSRVITAGKKFIEGQSTKLKDPRAQPGQSSPKIDVV 199
 QY 182 ISEASSNNLTDPGCTVFEDSELADTVANFTAFVPSIRQRLNLSGVTLTDTTEVTY 241
 Db 200 ISEASSNNLTDPGCTVFEDSELADTVANFTAFVPSIRQRLNLSGVTLTDTTEVTY 259
 QY 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINVDYLQSLKYYVGHGAGNPLGPTQGVY 301
 Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINVDYLQSLKYYVGHGAGNPLGPTQGVY 319
 QY 302 ANELIARLTHSPVHDDTSSNHTLDSSPATFPPLNSTLYADFSHDNGIISILFALGLYNGTK 361
 Db 320 ANELIARLTHSPVHDDTSSNHTLDSSPATFPPLNSTLYADFSHDNGIISILFALGLYNGTK 379
 QY 362 PLSTTTVENTITQTDGSSAWTVFPASRLYYEMMQCAEQEPLVRVLVNDVRVPLHGCPCVD 421
 Db 380 PLSTTTVENTITQTDGSSAWTVFPASRLYYEMMQCAEQEPLVRVLVNDVRVPLHGCPCVD 439
 QY 422 ALGRCRDSFVRGLSFARSGGDWAE 449
 Db 440 ALGRCRDSFVRGLSFARSGGDWAE 467

DA BVC

acid phosphatase (EC 3.1.3.2) repressible, precursor - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: acid phosphatase PHO5; protein YBR0814; protein YBR093c
C;Species: *Saccharomyces cerevisiae*
C;Date: 19-Feb-1984 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C;Accession: S05795; S38792; S48260; S45961; A00777; A38793; S41855; B25241; A25367; A27
R;Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinzen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A;Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A;Reference number: S05794; MUID:85037940; PMID:6093051
A;Accession: S05795
A;Molecule type: DNA
A;Residues: 1-467 <BAJ>
A;Cross-references: UNIPROT:P00635; EMBL:X01079; NID:g4162; PIDN:CAA25555.1; PID:g758282
A;Note: the authors translated the codon TAC for residue 272 as Thr
A;Accession: A38792
A;Molecule type: protein
A;Residues: 18-45 <BAJ2>
R;Mannhaupt, G.; Stucka, R.; Ehnlé, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A;Reference number: S48255; MUID:95208357; PMID:7900426
A;Accession: S48260
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-467 <WAN>
A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55598.1; PID:g476051
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R;Feldmann, H.; Mannhaupt, G.; Schwarzlöse, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45927
A;Accession: S45961
A;Molecule type: DNA
A;Residues: 1-467 <PE2>
A;Cross-references: EMBL:Z35962; NID:9536364; PIDN:CAA85046.1; PID:g5336365; GSPDB:GN0000
R;Arima, K.; Oshima, T.; Kubota, I.; Nakamura, N.; Mizunaga, T.; Toh-e, A.
Nucleic Acids Res. 11, 1657-1672, 1983
A;Title: The nucleotide sequence of the yeast PHO5 gene: a putative precursor of repress
A;Reference number: A00777; MUID:83168913; PMID:6300772
A;Accession: A00777
A;Molecule type: DNA
A;Residues: 1-35, 'Y', 37-129, 'G', 131-293, 'Q', 295-445, 'V', 447-461, 'DT', 464-465, 'K', 467 <AR
A;Cross-references: EMBL:V01320; NID:g4158; PIDN:CAA24630.1; PID:g4159
A;Accession: A38793
A;Molecule type: protein
A;Residues: 18-26, 'X', 28 <ARI2>
R;Meyhack, B.; Bajwa, W.; Rudolph, H.; Hinzen, A.
EMBO J. 1, 675-680, 1982
A;Title: Two yeast acid phosphatase structural genes are the result of a tandem duplicat
A;Reference number: S41855; MUID:84236032; PMID:6329697
A;Accession: S41855
A;Molecule type: DNA
A;Residues: 1-30, 'T', 32-51, 'S', 53-75 <MEY>
A;Cross-references: EMBL:M24178; NID:g172156; PIDN:AAA34868.1; PID:g172157
R;Tail-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Hostian, S.J.; Thill, G.
Mol. Cell. Biol. 6, 1855-1865, 1986
A;Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within
A;Reference number: A93074; MUID:87064474; PMID:3537710
A;Accession: B25241
A;Molecule type: DNA
A;Residues: 1-44 <TAI>
R;Bergman, L.W.
Mol. Cell. Biol. 6, 2298-2304, 1986
A;Title: A DNA fragment containing the upstream activator sequence determines nucleosome
A;Reference number: A25367; MUID:87064526; PMID:3023927
A;Accession: A25367
A;Molecule type: DNA
A;Residues: 1-2, 'Y', 4-43, 'T', 45-51 <BER>
R;Silve, S.; Monod, M.; Hinzen, A.; Haguenaier-Tsapis, R.
Mol. Cell. Biol. 7, 3306-3314, 1987

A;Title: The yeast acid phosphatase can enter the secretory pathway without its N-terminus

A;Reference number: A27774; MUID:89038886; PMID:3313013

A;Accession: A27774

A;Molecule type: DNA

A;Residues: 1-51,'S',53-60 <SIL>

A;Cross-references: GB:M17306

C;Genetics:

A;Gene: SGD:PHO5; MIPS:YBR093c

A;Cross-references: SGD:S0000297; MIPS:YBR093c

A;Map position: 2R

A;Note: YBR093c

C;Superfamily: yeast acid phosphatase

C;Keywords: glycoprotein; phosphonastidine; phosphoprotein; phosphoric monoester hydrolase

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-467/Product: acid phosphatase, repressible #status experimental <MAT>

F;75/Active site: His (phosphonastidine intermediate) #status predicted

F;97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (covalent)

F;337/Active site: His #status predicted

Query Match 16.3%; Score 385; DB 1; Length 467;

Best Local Similarity 26.2%; Pred. No. 2.4e-20;

Matches 114; Conservative 66; Mismatches 189; Indels 66; Gaps 14;

QY 31 GQVAPFSLANESVTPVPAGCRVTFQVLSRHGARYTDSKGYKSALIEISIQNATT 90

DB 42 GGAGFYYSFGDYGISRDLPCECMKQLQWGRHGERYPTVSLAKTIKSTWYKLSNYTRQ 101

QY 91 FDGKYATLK-TYNSLSGADD-----LTPF-GEQELVNSGIKFORYESLTR 134

DB 102 FNGSLSFNDDEYFEIRDDDLLEMTTANSDDVLNPTYGEMNAKHARDFLAQYGMVE 161

QY 135 NIVPFF-IRSGSSRVIASGKKFIEGFQSTKLADPRAQSQSPKIDVISEASSNNITLD 193

DB 162 NQTSFAVFTSNKSRCHDTAQYFIDG-----LGD-----QENITLQTVSEASAGANTLS 210

QY 194 P-GTCTVPESELADTVANFTATVPISIRQKLENDLSGVTITDTEVYIMDCSPFTIS 252

DB 211 ACNSCPAW-DYDANDDI VNEYDITYLDIDIAKLKENKGLNLTSTASTILFSWCAFE-- 266

QY 253 TSTVDYTK-LSPFCDLFTHDEMINVDYLOSLLKYYGHGAGNPLGPTOGVGVANELIARLTH 311

DB 267 ---VNAKGYSDVCDIFTKDELVLHYSYYQDLHTYVHEHGPYDIIKSVGSNLFNASVKLLKQ 323

QY 312 SPVHDDTSSNHTLDS SPATFLNLSYADFSDHNGIISILFALGLYNGTKPLSTTTVENI 371

DB 324 SEIQD-----QKVLSTFHTDITLNFELTTAGIIDDKNNLTAEYVPEM 365

QY 372 TQTDGFSANTVPASRLYVEMQCAQEPILVRVLVNDVRVPLHGCPVDALGRCTRDSF 431

DB 366 GNT--FHRSMWVPOGARVYTEKFQC--SNDTYRVYVINDAVVPIETCTGPGFSCEINDF 421

QY 432 -----VRGLSEAR 439

DB 422 YDVAEKVAVAGTDFLK 436

RESULT 5

PABCC

A;Title: The yeast acid phosphatase (EC 3.1.3.2) precursor, constitutive - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: acid phosphatase PHO3; protein YBR0813; protein YBR092c

C;Species: *Saccharomyces cerevisiae*

C;Date: 30-Sep-1991 #sequence revision 09-Sep-1994 #text_change 09-Jul-2004

C;Accession: S48259; S45960; S05794; A25241; S44674

R;Yannhaupt, G.; Stucka, R.; Ehle, S.; Vetter, I.; Feldmann, H.

Yeast 10, 1363-1381, 1994

A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.

A;Reference number: S48255; MUID:95208357; PMID:7900426

A;Accession: S48259

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-467 <MAN>

A;Cross-references: UNIPROT:P24031; EMBL:X78993; NID:X476045; PIDN:CAA55597.1; PID:G47601

A;Note: the nucleotide sequence was submitted to the EMBL Data Library April 1994

R;Pelkmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45927
A;Accession: S45960
A;Molecule type: DNA
A;Residues: 1-467 <FE2>
A;Cross-references: EMBL:Z35961; NID:G536362; PIDN:CAA85045.1; PID:G536363; GSPDB:GN0000
R;Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A;Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A;Reference number: S05794; MUID:85037940; PMID:6093051
A;Accession: S05794
A;Molecule type: DNA
A;Residues: 1-218, 'NKT', 222-467 <BAJ1>
A;Cross-references: EMBL:X01080; NID:G4148; PIDN:CAA25557.1; PID:G758281
A;Note: the authors translated the codon AAT for residue 134 as Asp and Trp for residue
R;Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G.
Mol. Cell. Biol. 6, 1855-1865, 1986
A;Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within
A;Reference number: A93074; MUID:87064474; PMID:3537710
A;Accession: A25241
A;Molecule type: DNA
A;Residues: 1-44 <TAI>
C;Genetics:
A;Gene: SGD:PHO3; MIPS:YBR092C
A;Cross-references: SGD:S0000296; MIPS:YBR092C
A;Map position: 2R
C;Superfamily: yeast acid phosphatase
C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-467/Product: acid phosphatase, constitutive #status predicted <MAT>
F;75/Active site: His (phosphohistidine intermediate) #status predicted
F;97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (coval
F;337/Active site: His #status predicted
Query Match 16.3%; Score 385; DB 1; Length 467;
Best Local Similarity 26.1%; Pred. No. 2.4e-20;
Matches 113; Conservative 63; Mismatches 195; Indels 62; Gaps 11;
Qy 31 GQVAPFSLANESVISPEVAGCRVTFQAQVLSRHGARYPTDSKGYKYSALIEBIOQNATT 90
Db 42 GGAGPYFSPGDIYISRDLEPGCEMKQLQMLARHGERTYPTYSKATIMTKYKLSNYTRQ 101
Qy 91 FDGKYAFK-TYNSVLCADD-----LTPF-GEQELVNSGKIFKYORYESLTR 134
Db 102 FNGSLFLNDYDFEIRDDDDLEMETTFANSNDVLPYTGEMAKRHAREFLAQGYMFE 161
Qy 135 NIVVPF-IRSSGSRVITAGSKKFIIEGQSTKLDKPAQPGQSSPKIDVIVISEASSNNTLD 193
Db 162 NQTSFPIFAASSRVHDTAQYFIDG-----LGD-----QFNISLQTVSEAMGAGANTLS 210
Qy 194 PGCTVPEDSELADTVENATFATFVPSIRQRLNDSLGVTLTDTTEVTYLMDCSFDTIST 253
Db 211 AGNACPGWDEANDDILDKYDTTLLDIAKLNKENKGLNLTAKDANTLFAWCAYELNAR 270
Qy 254 STVDTKLSPPCDLFTDHEWNYDYLSQSLKYYGHGAGNPLGPTQGVGYANELLARTHSP 313
Db 271 GYSDV-----CDLFTDELVRYSYQDLVSYQDGPYDMIRSVGANLFWATLKLKQSE 325
Qy 314 VHDTSNHTLDSPPATFPLNSTLYADFSHNGIISILFALGLYNGTKPKLSTTTVENITQ 373
Db 326 TQD-----LKVLSFTHTDITLNYLTLAGITDDKNLNTAEYVPPMGN 367
Qy 374 TDGFSASWTPFASRLVEMVQCAEQEPLVRLVNDRVPLHGPCPVDALGRCTRDSF-- 431
Db 368 T--FKSWYVPGARVYTEKFQC--SNDTVRVVINDAVVPIETCTCTGPGFSCEINDFYD 423
Qy 432 -----VRGLSFAR 439
Db 424 YAEKRVAGTDFLK 436

RESULT 6

S52495
acid phosphatase homolog YDL024C - Yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D2815
C;Species: Saccharomyces cerevisiae
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52495; S67556
R;Andre, B.; Visser, S.; Urrestazu, L.
submitted to the EMBL Data Library, February 1995
A;Description: The sequence of a 42 kb segment located on the left arm of chromosome IV
A;Reference number: S52492
A;Accession: S52495
A;Molecule type: DNA
A;Residues: 1-468 <AND>
A;Cross-references: UNIPROT:P52290; EMBL:Z48432; NID:G683669; PIDN:CAA88335.1; PID:G68366
R;Urrestazu, L.A.; Andre, B.; Visser, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67535
A;Accession: S67556
A;Molecule type: DNA
A;Residues: 1-468 <URR>
A;Cross-references: EMBL:Z74072; NID:G1430996; PIDN:CAA98583.1; PID:G1430997; MIPS:YDL024
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:DIA3
A;Cross-references: SGD:S0002182
A;Map position: 4L
C;Superfamily: yeast acid phosphatase
Query Match 15.6%; Score 368; DB 2; Length 468;
Best Local Similarity 25.0%; Pred. No. 4.2e-19;
Matches 109; Conservative 74; Mismatches 181; Indels 72; Gaps 13;
Qy 31 GQVAPFSLANESVISPEVAGCRVTFQAQVLSRHGARYPTDSKGYKYSALIEBIOQNATT 90
Db 43 GGSAPYFSPGDIYISRDLEPGCRLLTQVQMTGRHGERYPTRSEAKDIFEVYKISNYTKG 102
Qy 91 FDGKYAFKLT-TYNSVLCADD-----GADDLTPF-GEQELVNSGKIFKYORYESLTR 134
Db 103 YEGSLFLNDYDFEIRDDDDLEMETTFANSNDVLPYTGEMAKRHAREFLAQYKLMFE 162
Qy 135 NIVVPF-IRSSGSRVITAGSKKFIIEGQSTKLDKPAQPGQSSPKIDVIVISEASSN 189
Db 163 NCTNFFIFTNSKRIYDTAQYFAEALDGDGNIS-----LQTLSENSSGA 207
Qy 190 NTLDPGCTVPEDSELADTVENATFATFVPSIRQRLNDSLGVTLTDTTEVTYLMDCSPD 249
Db 208 NTLAAKSSCPNWNNSANNNDILMSYSDYLENIDRLNENKGNLSKDKDAALFSCWAFE 267
Qy 250 TISTSTVDYTK-LSPFCDLFTDHEWNYDYLSQSLKYYGHGAGNPLGPTQGVGYANELLAR 308
Db 268 -----LNAGYGNICDIFSAELIHYSYETDLTSFYQNGPYKLIKISGANLFWATV-X 320
Qy 309 LTHSPVHDDTSNHTLDSPPATFPLNSTLYADFSHNGIISILFALGLYNGTKPKLSTTTV 368
Db 321 LIRQSAH-----LBQKVLWSFTHTDITLNYLTLAGITDDTNLTNNHV 363
Qy 369 ENITQDGFSSAWTPFASRLVEMVQCAEQEPLVRLVNDRVPLHGPCPVDALGRCTR 428
Db 364 P--FRDHSYHRSWYVPGARVYTEKFQC--SNDSYRVVNDVAVFIESCSSGPGFSCEE 419
Qy 429 DSF-----VRGLSF 437
Db 420 GTFVEYAKDLRLGVSF 435
RESULT 7
S48996
acid phosphatase (EC 3.1.3.2) PHO12 - Yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YHR215W
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: S48996; S59659

R;Macri, C.
 submitted to the EMBL Data Library, February 1994
 A;Description: The sequence of *S. cerevisiae* cosmid 9177.
 A;Reference number: S46671
 A;Accession: S48996
 A;Molecule type: DNA
 A;Residues: 1-467 <MAC>
 A;Cross-references: UNIPROT:P38693; EMBL:U00029; NID:g551322; PIDN:AA69729.1; PID:g4589
 R;Xu, L.
 submitted to the EMBL Data Library, January 1995
 A;Reference number: S59658
 A;Accession: S59659
 A;Molecule type: DNA
 A;Residues: 1-16, 'L', 18-81, 'AR', 84-149, 'H', 151-467 <XUL>
 A;Cross-references: EMBL:U19789; NID:g847754; PIDN:AAA73479.1; PID:g847755
 C;Genetics:
 A;Gene: SGD:PHO12
 A;Cross-references: SGD:S0001258; MIPS:YHR215W
 A;Map position: 8R
 C;Superfamily: yeast acid phosphatase
 C;Keywords: phosphoric monoester hydrolase

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Query Match          14.9%; Score 352; DB 2; Length 467;
Best Local Similarity 24.4%; Pred. No. 6.1e-18;
Matches 107; Conservative 70; Mismatches 189; Indels 72; Gaps 14;

QY 31 GQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARYPTDSKGKYSALIEEIQONATT 90
Db 42 GSGPYVFPDGYGISRDLPESCEMKQVMGRHGERPTTVSKAKSINTWYKLSNYTGG 101

QY 91 FDGKYAFILK-----TNYSL-----GADDLTPF-GEQELVNSGIKFYQYESLTR 134
Db 102 FSGALSFLNDDYEFPIRDTKNLEMETTLANSVNVLPYTGEMNAKRHARDFLAQGYMVE 161

QY 135 NIVPP-IRSSGSRVIAAGKFIQGFQSTKLDPRAQPGQSSPKIDV---VISEASSN- 189
Db 162 NQTSFAVFTSNRCHDTAQYFIDGL-----GDKFNIQLQITISEAESAGA 206

QY 190 NTLDP-GCTCTVFESSELAETVEANFTATFVPSIRORLENDLSGVTLTDTETVYLMDCSF 248
Db 207 NTLNHAHSCPAWDD-DVNDLILKDYTKYLSGIARLNKENKGLNLTSSDANTFFAWCAY 265

QY 249 DTISTSTVDTKLSPCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVGYANELIAR 308
Db 266 EINARG-----YSDICNIFTKDELVRFSYGQDLETYYQTGPGYDVVRSGANLFNASVKL 320

QY 309 LTHSPVHDDTSSNHTLSDSPATFPLNSTLYADPSHDNGIISILFALGLYNGTKPLSTTTV 368
Db 321 LKSEVQD-----QKWLSTHTDITLNYLTITIGIIDDQNNTLTAHV 362

QY 369 ENITQTDGFSAWTVPFASRLYVEMMQCAEQEPLRVLVNDRVPLHGCVPDALGRCTR 428
Db 363 PFMENT--FHSWVYVPGQARVYTEKFC--SNDIVRVVINDAVVPIETCTSGPGFSCEI 418

QY 429 DSP-----VRGLSFAR 439
Db 419 NDFYGYAEKRVAGTDFLK 436

```

RESULT 8
 S53476
 acid phosphatase [EC 3.1.3.2] precursor - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: protein YAR071w
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C;Accession: S53476; JCI018
 R;Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Kabac
 submitted to the EMBL Data Library, February 1994
 A;Description: Sequencing of chromosome I of *Saccharomyces cerevisiae*: analysis of the 5
 A;Reference number: S53458
 A;Accession: S53476
 A;Molecule type: DNA
 A;Residues: 1-467 <BUS>

A;Cross-references: UNIPROT:P35842; EMBL:L28920; NID:g1616966; PIDN:AAC09508.1; PID:g4561
 R;Chen, J.Y.; Gong, Y.; Ao, S.Z.
 Acta Biochim. Biophys. Sin. 21, 437-444, 1989
 A;Title: The primary structure of acid phosphatase gene PHO11 in *S. cerevisiae* and compa
 A;Reference number: JCI018
 A;Accession: JCI018
 A;Molecule type: DNA
 A;Residues: 1-16, 'L', 18-149, 'H', 151-353, 'O', 355-422, 'G', 424-467 <CHE>
 A;Note: this paper is in Chinese, with an English abstract
 C;Genetics:
 A;Gene: SGD:PHO11
 A;Cross-references: SGD:S0000094; MIPS:YAR071w
 A;Map position: 1R
 C;Superfamily: yeast acid phosphatase
 C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
 F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-467/Product: acid phosphatase #status predicted <MAT>
 F;74/Active site: Arg #status predicted
 F;75/Active site: His (phosphohistidine intermediate) #status predicted
 F;97,162,192,250,315,356,439,445,461/Binding site: carboxylate (Asn) (covalent) #status

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Query Match          14.9%; Score 352; DB 2; Length 467;
Best Local Similarity 24.4%; Pred. No. 6.1e-18;
Matches 107; Conservative 70; Mismatches 189; Indels 72; Gaps 14;

QY 31 GQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARYPTDSKGKYSALIEEIQONATT 90
Db 42 GSGPYVFPDGYGISRDLPESCEMKQVMGRHGERPTTVSKAKSINTWYKLSNYTGG 101

QY 91 FDGKYAFILK-----TNYSL-----GADDLTPF-GEQELVNSGIKFYQYESLTR 134
Db 102 FSGALSFLNDDYEFPIRDTKNLEMETTLANSVNVLPYTGEMNAKRHARDFLAQGYMVE 161

QY 135 NIVPP-IRSSGSRVIAAGKFIQGFQSTKLDPRAQPGQSSPKIDV---VISEASSN- 189
Db 162 NQTSFAVFTSNRCHDTAQYFIDGL-----GDKFNIQLQITISEAESAGA 206

QY 190 NTLDP-GCTCTVFESSELAETVEANFTATFVPSIRORLENDLSGVTLTDTETVYLMDCSF 248
Db 207 NTLNHAHSCPAWDD-DVNDLILKDYTKYLSGIARLNKENKGLNLTSSDANTFFAWCAY 265

QY 249 DTISTSTVDTKLSPCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVGYANELIAR 308
Db 266 EINARG-----YSDICNIFTKDELVRFSYGQDLETYYQTGPGYDVVRSGANLFNASVKL 320

QY 309 LTHSPVHDDTSSNHTLSDSPATFPLNSTLYADPSHDNGIISILFALGLYNGTKPLSTTTV 368
Db 321 LKSEVQD-----QKWLSTHTDITLNYLTITIGIIDDQNNTLTAHV 362

QY 369 ENITQTDGFSAWTVPFASRLYVEMMQCAEQEPLRVLVNDRVPLHGCVPDALGRCTR 428
Db 363 PFMENT--FHSWVYVPGQARVYTEKFC--SNDIVRVVINDAVVPIETCTSGPGFSCEI 418

QY 429 DSP-----VRGLSFAR 439
Db 419 NDFYGYAEKRVAGTDFLK 436

```

RESULT 9
 JN0715
 3-phytase [EC 3.1.3.8] B precursor - *Aspergillus ficum*
 N;Alternate names: pH 2.5-optimum acid phosphatase
 C;Species: *Aspergillus ficum*
 C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
 C;Accession: JN0715; P05994; P0460
 R;Ehrlich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J.
 Biochem. Biophys. Res. Commun. 195, 53-57, 1993
 A;Title: Identification and cloning of a second phytase gene (phyB) from *Aspergillus nigr*
 A;Reference number: JN0715; MUID:93371452; PMID:7916610
 A;Accession: JN0715
 A;Molecule type: DNA
 A;Residues: 1-479 <EHR>
 A;Cross-references: UNIPROT:P81440; GB:L20567

A;Accession: PN0594
A:Molecule type: protein
A:Residues: 20-101;133-146;376-399 <RH2>
R;Ullah, A.H.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 192, 754-759, 1993
A;Title: Identification of active-site residues in *Aspergillus ficuum* extracellular pH 2
A;Reference number: PN0460; MUID:93249452; PMID:8484781
A;Accession: PN0460
A:Molecule type: protein
A:Residues: 65-66,68-93 <ULL>
C;Comment: This enzyme, previously characterized as an acid phosphatase (EC 3.1.3.2), hydrolyzes
C;Genetics:
A;Gene: phbB
A;Introns: 261/1; 300/2; 335/2
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phospho
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-479/Product: 3-phytase #status experimental <MAT>
F;81,337/Active site: Arg, His #status predicted
F;92/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #status
Query Match 14.4%; Score 339.5; DB 1; Length 479;
Best Local Similarity 27.0%; Pred. No. 5.2e-17;
Matches 118; Conservative 64; Mismatches 186; Indels 69; Gaps 19;
QY 3 AVPASRNQSS-CTVDQGYQCFSETSHLWQYAPFFSLANESV---ISPEVPAGCRVTFA 58
Db 25 AIPQSTQEKQFSQEFRDGYSILKH-----YGGNGPY----SERVSYGIARDPPTSCHEVDQV 76
QY 59 QVLSRHGARYPTDSKGGKY-SALIEEIQQNATTFDCKYAFKTYNYSL-----GADDLT 111
Db 77 IMVRHGERYPSPSAGKDIIEALAKVYSINTTEYKGLDFLNDWTYYVNECYNAETTS 136
QY 112 -PF-GEQELVNSGKIFQRYESL--TRNIYVPIRSSGSSRVIASGKFFIEGFQSTKLKDP 167
Db 137 GPYAGLLDAVNHGNDYKARYGHLWNGETVVPFF--SSGYGRVETARKFGEGFGYNY--- 192
QY 168 RAQPGQSSPKIDVISEASSNNITLDPGCTVPEDESELADTVEANFTATVPSTQRLEN 227
Db 193 -----STNAALNTISESEVMGADSLTP--TCDDNDQTTCDNLTYQLPQFKVAARLNSQN 246
QY 228 DLGVTLTDTETVYLMDCSFDITSTVDTKLSPPCDFTHDEWINDYLSLKKYYGH 287
Db 247 --PGMNLITASDVNLMVMASFEINA-----RPSNWINAFTQDEWVSGFVEDLNYYYCA 299
QY 288 GAGNPLGPTQGVYANELIARLTHSPVHDHTSSNHTLDSSPATFPLNSTLYADPSSHNGI 347
Db 300 GPQDKNMAVAVYANASLTLLNQGP-----KEAGP-----LFFNLADHTNI 341
QY 348 ISILFALGLY--NGTKPLSTTTVENTITQDGFSSAWTPFASRLYVEMMOCA-----EQE 401
Db 342 TPILAALGVLPNEDELPLDRVAFGN-----PYSIGNIVPMGGHLLTIERLSQATALSDEK 396
QY 402 PLVRLVNDRAVPLHGC 418
Db 397 TYVRLVNEAVLPND 413
RESULT 10
JN0890
acid phosphatase (EC 3.1.3.2) precursor - *Aspergillus awamori*
C;Species: *Aspergillus awamori*
C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
R;Piddington, C.S.; Houston, C.S.; Palohelmo, M.; Cantrell, M.; Miettinen-Oinonen, A.; N
Gene 133, 55-62, 1993
A;Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-opti
A;Reference number: JN0889; MUID:94040796; PMID:8224894
A;Accession: JN0890
A:Molecule type: DNA
A:Residues: 1-479 <PID>
A;Cross-references: UNIPROT:P34755; GB:L02420; NID:g166481; PIDN:AAA16897.1; PID:g166482

A;Experimental source: strain ALX0243
C;Comment: The highly similar enzyme from *A. ficuum* has been shown to have 3-phytase (EC
C;Genetics:
A;Gene: aph
A;Introns: 261/1; 300/2; 335/2
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-479/Product: 3-phytase #status predicted <MAT>
F;81,337/Active site: Arg, His #status predicted
F;92/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #status
Query Match 14.4%; Score 338.5; DB 1; Length 479;
Best Local Similarity 26.8%; Pred. No. 6.1e-17;
Matches 117; Conservative 63; Mismatches 188; Indels 69; Gaps 18;
QY 3 AVPASRNQSS-CTVDQGYQCFSETSHLWQYAPFFSLANESV---ISPEVPAGCRVTFA 58
Db 25 AIPQSTQEKQFSQEFRDGYSILKH-----YGGNGPY----SERVSYGIARDPPTSCHEVDQV 76
QY 59 QVLSRHGARYPTDSKGGKY-SALIEEIQQNATTFDCKYAFKTYNYSL-----GADDLT 111
Db 77 IMVRHGERYPSPSAGKDIIEALAKVYSINTTEYKGLDFLNDWTYYVNECYNAETTS 136
QY 112 -PF-GEQELVNSGKIFQRYESL--TRNIYVPIRSSGSSRVIASGKFFIEGFQSTKLKDP 167
Db 137 GPYAGLLDAVNHGNDYKARYGHLWNGETVVPFF--SSGYGRVETARKFGEGFGYNY--- 192
QY 168 RAQPGQSSPKIDVISEASSNNITLDPGCTVPEDESELADTVEANFTATVPSTQRLEN 227
Db 193 -----STNAALNTISESEVMGADSLTP--TCDDNDQTTCDNLTYQLPQFKVAARLNSQN 246
QY 228 DLGVTLTDTETVYLMDCSFDITSTVDTKLSPPCDFTHDEWINDYLSLKKYYGH 287
Db 247 --PGMNLITASDVNLMVMASFEINA-----RPSNWINAFTQDEWVSGFVEDLNYYYCA 299
QY 288 GAGNPLGPTQGVYANELIARLTHSPVHDHTSSNHTLDSSPATFPLNSTLYADPSSHNGI 347
Db 300 GPQDKNMAVAVYANASLTLLNQGP-----AGSLFFNPAHDTNI 341
QY 348 ISILFALGLY--NGTKPLSTTTVENTITQDGFSSAWTPFASRLYVEMMOCA-----EQE 401
Db 342 TPILAALGVLPNEDELPLDRVAFGN-----PYSIGNIVPMGGHLLTIERLSQATALSDEG 396
QY 402 PLVRLVNDRAVPLHGC 418
Db 397 TYVRLVNEAVLPND 413
RESULT 11
JN4285
acid phosphatase (EC 3.1.3.2) precursor - yeast (*Pichia pastoris*)
N;Alternate names: orthophosphoric-monoester phosphohydrolase (acid optimum); Pho
C;Species: *Pichia pastoris*
C;Date: 14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JN4285
R;Payne, W.E.; Gannon, P.M.; Kaiser, C.A.
Gene 163, 19-26, 1995
A;Title: An inducible acid phosphatase from the yeast *Pichia pastoris*: Characterization
A;Reference number: JN4285; MUID:96001238; PMID:7557473
A;Accession: JN4285
A:Molecule type: DNA
A:Residues: 1-468 <PAY>
A;Cross-references: UNIPROT:P52291; GB:U28658; NID:g881955; PIDN:AAA85503.1; PID:g881956
A;Experimental source: GS115
C;Genetics:
A;Gene: phoI
C;Superfamily: yeast acid phosphatase
C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydroly
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-468/Product: acid phosphatase #status predicted <MAT>
F;84/Active site: His (phosphohistidine intermediate) #status predicted

QY 250 TISTSTVDTKLSFCDLTHDEWINDYLCSLKXKYGAGNPLGPTQGVYANELLARL 309
Db 268 IAIKHS-----FCSIFTPSEFLNFEYDSLDQAAYGGGPVSEWASTLGGAYINNA--- 319
QY 310 THSPVHDDTSSNHTLSSPATFLNLTLYADFGHNGIISILFALGLYNGTKPLSTTTVE 369
Db 320 -----DSLENVT---NP---DFDRKVFLAFTHDSNLIIPVEALGFFPDITQNPPLPTD 366
QY 370 NITQTDGSSAWTVFPASRLYVENMOQAEQEPFLVRVLRVNDVRVPLHGC 418
Db 367 KNIYTVSQKTSFVPAGNLITELFFC-SDSKYVVRHLVNRQVYPLTDC 414

RESULT 14
S14119
acid phosphatase (EC 3.1.3.2) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S14119; T40455
R;Yang, J.; Schweingruber, M.E.
Curr. Genet. 18, 269-272, 1990
A;Title: The structural gene coding for thiamin-repressible acid phosphatase in Schizosaccharomyces pombe
A;Reference number: S14119; MUID:91064763; PMID:2249257
A;Accession: S14119
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-463 <YAN>
A;Cross-references: UNIPROT:Q01682; GB:X56939; NID:g5006; PIDN:CAA40258.1; PID:g5007
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z21931
A;Accession: T40455
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-463 <YAN>
A;Cross-references: EMBL:AL034382; PIDN:CAA22278.1; GSPDB:GN00067; SPDB:SPBC428.03c
A;Experimental source: strain 972h-; cosmid c428
C;Genetics:
A;Gene: SPBC428.03c
A;Map position: 2
C;Superfamily: yeast acid phosphatase
C;Keywords: phosphoric monoester hydrolase

Query Match 12.08; Score 284; DB 2; Length 463;
Best Local Similarity 24.94; Pred. No. 5.5e-13;
Matches 102; Conservative 66; Mismatches 181; Indels 60; Gaps 13;
QY 33 YAPFSLANBSVISPEVPAGCRVTFQAQLSRHGARYP-----TDSKGGKYSALIE--- 82
Db 43 HEFYENGPTTS-----FPESCAIKQVHLLQRHGSRNPTGDDTATDVSSAQYIDIFQNKLL 97
QY 83 --EIQQNAITFDGKIAFLKYNYSL---GADDLTPFGQEQLVNSGKIFQYORYSLTRNIV 137
Db 98 NGSTIPVNFSPENPLYEVKHWTPVKAENADQLSSGRIELFDLGRVFRYRYELFTDV 157
QY 138 PFTRSSGSSVIASGKXKFIQFQSTKLKDPRAQGGQSSPKIDVVI---SEASSNNLTDP 194
Db 158 YDINTAAQERVDSAEWFSYGMFGDDMON-----KTNFIVLDEDSAGANSAMY 207
QY 195 GTCTVFEDSEL-ADTVEANETA---TFVPSIRQLENDL-SGVTLTDTVTYLMDCMSFD 249
Db 208 YSCPVEDNNIDENTTEAHTSWENVFLKPIANLNKYFDSGYNLTVSDVRSLYICVYE 267
QY 250 TISTSTVDTKLSFCDLTHDEWINDYLCSLKXKYGAGNPLGPTQGVYANELLARL 309
Db 268 IALRDNDS-----FCSLFTSEFLNFEYDSLDQAAYGGGPVSEWASTLGGAYINNA--- 322
QY 310 THSPVHDDTSSNHTLSSPATFLNLTLYADFGHNGIISILFALGLYNGTKPLSTTTVE 369
Db 323 R-----KGVNNSDRK-----VFIAFTHDSQLIPVEALGFFPDITPHEPLPTD 366
QY 370 NITQTDGSSAWTVFPASRLYVENMOQAEQEPFLVRVLRVNDVRVPLHGC 418

Db 367 KNIYTVSLKTSFVPAGNLITELFFC-SDKNKYVVRHLVNRQVYPLTDC 414

RESULT 15
A86233
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86233
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86233
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-468 <STO>
A;Cross-references: UNIPROT:O04509; GB:AE005172; NID:g2160177; PIDN:AAB60740.1; GSPDB:GM000000000
C;Genetics:
A;Map position: 1
C;Superfamily: yeast acid phosphatase

Query Match 6.3%; Score 148; DB 2; Length 468;
Best Local Similarity 21.8%; Pred. No. 0.0047;
Matches 100; Conservative 60; Mismatches 202; Indels 96; Gaps 19;
QY 16 VDQYQCFSETSL--WGQYAPFSLANBSVISPEVPAGCRVTFQAQLSRHGARYP--- 70
Db 16 VSQADQGFDRHSLTVTRYSTSKDVTQNLIEGNNVSECTPIHLNLVAHGRTRSPTKR 75
QY 71 ----DSKGGKYSALIEEIQQNAITFDGKIAFL---KTNYSLGADDLTPFGQEQLVNSG 122
Db 76 LRELSLAGRFKELVRDAEARKLPDSKIPGWLQWKSFWEGKVGKGLIRQGEDELYQLG 135
QY 123 IKFYQRYESLTRN---IVFPIRSSGSSRVIASGKXKFIQFQSTKLKDPRAQGGQSSPKI 178
Db 136 IRVREPFPSLFEDYHPDVYTRATQIPRASASAVAFGMGLFSEK---GNLGFGRN--RA 190
QY 179 DVVISASSNNVLDPCTCTVFEDS-----ELADTVEANFTATFVPSIRQLEND 228
Db 191 FAVTSENRASTKLRFECQNTKYSYRKAKEPAVDKLEPVLNKITA----SVAKRYD-- 244
QY 229 LSGVTLTDTVTYLMDCMSFDTITSTVDTKLSFPFCDLFTHDEWINDYLCSLKXKYG 288
Db 245 ---LKFTKQDISLWFLCKQVALL-----EWTD-----DLEVPFLKG 278
QY 289 AGNPLGTCQGVYANELLARLTHSPVHDDT--SSNHTLSSPATFLNLTLYA--DFSHD 344
Db 279 YGNSLNYKMGV-----FILEDVLSHMEEAIKAREEKLPPGSEKARLRFABA 325
QY 345 NGIISILFALGLY-NGT-----KELSTTTVENITQTDGSSAWTVFPASRLYVENMQ 395
Db 326 ETIVPFPSCLGLFLDGSEFEKIOKEKPLELP--PQPKTRDFRGSTWAPFGNNILVYS 383
QY 396 COAQEQEP--LVRVLRVNDVRVPLHGCVPDVALGRCTRDSF 431
Db 384 CPAESSKYFQVVLNHEHPAVFGC--DGKDFCFLEDF 419

Search completed: October 24, 2004, 12:59:06
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